

STIC-Biotech/ChemLib

96007

From: Slobodyansky, Elizabeth
Sent: Friday, June 06, 2003 11:35 AM
To: STIC-Biotech/ChemLib
Subject: 09/800,187

Please search for case 09/800,187:

ED

SEQ ID NOS: 5 and 6 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652
CM1 10D11
703-306-3222

mail box 10D01

CREE

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
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Date Picked Up: 6/16/03
Date Completed: 6/16/03
Searcher Prep/Review: _____
Clerical: _____
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TYPE OF SEARCH:
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AA Sequences: _____
Structures: _____
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Full text: _____
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VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
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DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 03/02
WWW/Internet: _____
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ps Dislosure; fig 4; 116pp; English.

xx The present invention relates to novel histone deacetylase proteins and polynucleotides encoding them. Sequences of the invention are useful for identifying modulating agents that are used for preventing, ameliorating, treating or correcting dysfunctions or diseases such as cancer. They can also be used to screen for human histone deacetylase activators and inhibitors. They are useful for generating antibodies and can be used as bait proteins in two-hybrid assay or three-hybrid assay. The present sequence is human histone deacetylase 6 protein.

cc Sequence 1215 AA;

cc Query Match 100.0%; Score 6397; DB 23; Length 1215;

cc Best Local Similarity 100.0%; Pred. No. 0;

cc Matches 1215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MTSGQDSTTRQRSRQNPQSPQDSSVTSKRNIKKGAVPKRSIPPLAEVKKKKKKK 60
DB 1 MTSGQDSTTRQRSRQNPQSPQDSSVTSKRNIKKGAVPKRSIPPLAEVKKKKKKK 60
OY 61 QAMEEDLIVGLOGMDLNEAEALAGTGLVLDQLEFHCIMLMDSPPEGPERLAIKEOLI 120
DB 61 QAMEEDLIVGLOGMDLNEAEALAGTGLVLDQLEFHCIMLMDSPPEGPERLAIKEOLI 120
OY 121 QEGILDRCVSPQARAEKEELMLVHSLEYIDMETTYQNNEGELRYLADTYDSYLIHPS 180
DB 121 QEGILDRCVSPQARAEKEELMLVHSLEYIDMETTYQNNEGELRYLADTYDSYLIHPS 180
OY 181 YSCACLAGSVLRVDVAVGAETIRNGMATIRPPGHHAQSLMDGYCMFNHVAVAARYAQ 240
DB 181 YSCACLAGSVLRVDVAVGAETIRNGMATIRPPGHHAQSLMDGYCMFNHVAVAARYAQ 240
OY 241 KHRIRRVILVDMVHHGGTQFTPDQDSVLYFSIHRREQGRFWPLKASNNSTGFGG 300
DB 241 KHRIRRVILVDMVHHGGTQFTPDQDSVLYFSIHRREQGRFWPLKASNNSTGFGG 300
OY 301 QGYTINVMNOVGMDADYIAAFVHLVLPVLEFPOLVLAAGPDALOGDKGEMAAP 360
DB 301 QGYTINVMNOVGMDADYIAAFVHLVLPVLEFPOLVLAAGPDALOGDKGEMAAP 360
OY 361 AGFADLTHLMLAGLCKLILSLEGYNLRALAEVSAHLTLGDCPMLSEPGAPCRSA 420
DB 361 AGFADLTHLMLAGLCKLILSLEGYNLRALAEVSAHLTLGDCPMLSEPGAPCRSA 420
OY 421 QASVSCALELEPEFVETVLRSTETVERDMEEDNVEESEEGPWEPPVLPILTWYLOS 480
DB 421 QASVSCALELEPEFVETVLRSTETVERDMEEDNVEESEEGPWEPPVLPILTWYLOS 480
OY 481 TGLVYDMMNMHNCNMDSHHPVPRILRIMCRLEELAGRCILTLTPRPAEALITGH 540
DB 481 TGLVYDMMNMHNCNMDSHHPVPRILRIMCRLEELAGRCILTLTPRPAEALITGH 540
OY 541 SAEVGHILRATEKMTRELHRESSNFDSTIYICPSTFACQLATGAACRLVEAVLSEVYN 600
DB 541 SAEVGHILRATEKMTRELHRESSNFDSTIYICPSTFACQLATGAACRLVEAVLSEVYN 600
OY 601 GAAVVRPGRHAEODACGCFEFSVAVAAHQAQITSGHALRILIVDMVHHNGTQHM 660
DB 601 GAAVVRPGRHAEODACGCFEFSVAVAAHQAQITSGHALRILIVDMVHHNGTQHM 660
OY 661 EDDSVLVLSLHRYHGTFFPMGDGASQIGRAAGTGTVAVANNRPMGADYLAAMH 720
DB 661 EDDSVLVLSLHRYHGTFFPMGDGASQIGRAAGTGTVAVANNRPMGADYLAAMH 720
OY 721 RLVPILAEFNPDELVSAGFPAAGDPLGGCVSPREGAHLTHLMLGASRIILILEG 780
DB 721 RLVPILAEFNPDELVSAGFPAAGDPLGGCVSPREGAHLTHLMLGASRIILILEG 780
OY 781 GYNLTISSESMAACTRSLGDPPPLTLPRPLSGALASTETIGVHRRYRSLRYMKE 840
DB 781 GYNLTISSESMAACTRSLGDPPPLTLPRPLSGALASTETIGVHRRYRSLRYMKE 840

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OY 841 DREGSSSKLYTKKAPQAPRPAERNTREKVLNAGMKVYSASGEESTPGQTNSET 900
DB 841 DREGSSSKLYTKKAPQAPRPAERNTREKVLNAGMKVYSASGEESTPGQTNSET 900
OY 901 AVVALTODPSEATGATLAQTISEAIGAMIGQTTSEAVAGATPDQTTSEETVGA 960
DB 901 AVVALTODPSEATGATLAQTISEAIGAMIGQTTSEAVAGATPDQTTSEETVGA 960
OY 961 ILDTQTTSEAVGATLGQTTSEAVGATLAQTISEAMGATLDQTTSEAPGTGLIQ 1020
DB 961 ILDTQTTSEAVGATLGQTTSEAVGATLAQTISEAMGATLDQTTSEAPGTGLIQ 1020
OY 1021 TPLASTDQTPPTSPVQGTTPQISPSSTLIGSLRTLESGSSGASASQAPGENILGEA 1080
DB 1021 TPLASTDQTPPTSPVQGTTPQISPSSTLIGSLRTLESGSSGASASQAPGENILGEA 1080
OY 1081 AGGDMADSMLMGSGSLTFOALFYAVTPPLPMPCPHVAVCPIPAAGLDVTPCGDCGTIQ 1140
DB 1081 AGGDMADSMLMGSGSLTFOALFYAVTPPLPMPCPHVAVCPIPAAGLDVTPCGDCGTIQ 1140
OY 1141 ENMVCLSCYQVYCGRYINGHMLQHGNSGHPLVLSYIDLSAMCYCCQAYVHHQALDVK 1200
DB 1141 ENMVCLSCYQVYCGRYINGHMLQHGNSGHPLVLSYIDLSAMCYCCQAYVHHQALDVK 1200
OY 1201 IAHONKEGDMPPH 1215
DB 1201 IAHONKEGDMPPH 1215

RESULT 2
AAU99661
ID AAU99661 standard; protein; 1215 AA.
XX
AC AAU99661;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human histone deacetylase isoform 6.
XX
KW Human; histone deacetylase; HDAC-6; cancer; cytosolic;
KW antisenase; tumor suppressor; cell proliferation; tumor;
KW programmed cell death; necrotic cell death.
XX
OS Homo sapiens.
XX
FH Key
FH Location/Qualifiers
FT Misc-difference 171
FT /note- "Encoded by CAC"
FT Misc-difference 244
FT /note- "Encoded by ACC"
FT Misc-difference 334
FT /note- "Encoded by CTC"
FT Misc-difference 388
FT /note- "Encoded by CTC"
FT Misc-difference 410
FT /note- "Encoded by CCG"
FT Misc-difference 474
FT /note- "Encoded by CCG"
FT Misc-difference 512
FT /note- "Encoded by NGG"
FT /label= OTHER
FT /note= "represented as 0 in the specification. Encoded by TGC"
FT Misc-difference 519
FT /note= "Encoded by CCG"
FT Misc-difference 526
FT /note= "Encoded by CTG"
FT Misc-difference 581
FT /note= "Encoded by CTT"
FT Misc-difference 594
FT /note= "Encoded by CTC"
FT Misc-difference 599
FT /note= "Encoded by CTC"
FT Misc-difference 621
FT /note= "Encoded by CTG"

```

Query Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
99.5%;	99.2%;	6364;	23;	1215;	8;	2;	0;	0;	0;
Predicted No. of Mismatches: 0; Indels: 0; Gaps: 0									
<p>1 MTSNGODSTTTRORRSRONPOSPPDDSSVTSKRNTKKGAVPSITNLAEVKKKGMMKRLG 60</p> <p>1 MTSNGODSTTTRORRSRONPOSPPDDSSVTSKRNTKKGAVPSITNLAEVKKKGMMKRLG 60</p>									

QY	61	QAMEBDLYLGLQGMPLNLEAALACTGVLVDQOLNDFHCLMDSPSEGERHAIKEDLI	120
Db	61	QAMEBDLYLGLQGMPLNLEAALACTGVLVDQOLNDFHCLMDSPSEGERHAIKEDLI	120
QY	121	QEGLLDRCSFQARAEKEELMLVLSLEYIDIMETTYOYNBCELVLADTYDVLHPNS	180
Db	121	QEGLLDRCSFQARAEKEELMLVLSLEYIDIMETTYOYNBCELVLADTYDVLHPNS	180
QY	181	YSCACLAGSVLRVLDVAVLGAETIRNGMAIIRPPGHHAQSHLMDGYCMFNVAVAARYAQ	240
Db	181	YSCACLAGSVLRVLDVAVLGAETIRNGMAIIRPPGHHAQSHLMDGYCMFNVAVAARYAQ	240
QY	241	KRIRIRVLYVMDVHHGGTOFTPODPSVLYFESHREDOGRFPHILKASNMSTGFGOG	300
Db	241	KRIRIRVLYVMDVHHGGTOFTPODPSVLYFESHREDOGRFPHILKASNMSTGFGOG	300
QY	301	QGYTINVMNOCGMADADYIAAFHLVLLPVALFEPOLVVAAGFDALOGDPKGEMAAATP	360
Db	301	QGYTINVMNOCGMADADYIAAFHLVLLPVALFEPOLVVAAGFDALOGDPKGEMAAATP	360
QY	361	AGFAQLTHILMGLAGSKILLSEGGYNLRALAEVVSASLHTLLGDPCMLDESPGAPCRSA	420
Db	361	AGFAQLTHILMGLAGSKILLSEGGYNLRALAEVVSASLHTLLGDPCMLDESPGAPCRSA	420
QY	421	QASVSCALAELEPFMEVLYVRSFTEYERNMEDNDESEEBEPWBPVPLITLTPVLOS	480
Db	421	QASVSCALAELEPFMEVLYVRSFTEYERNMEDNDESEEBEPWBPVPLITLTPVLOS	480
QY	481	TGLVYDQNMNHCNMLDHPREVPORIRIMCRLEBELAGRCILTPRPATEALILCH	540
Db	481	TGLVYDQNMNHCNMLDHPREVPORIRIMCRLEBELAGRCILTPRPATEALILCH	540
QY	541	SAEYVGHRLATEKMKTRLEHRESSNFDSIYICPSTFACAOATGAACRLVEAVLSEVYN	600
Db	541	SAEYVGHRLATEKMKTRLEHRESSNFDSIYICPSTFACAOATGAACRLVEAVLSEVYN	600
QY	601	GAAYVRPBGHNAEDDAACGCFEPNSVVAANHAQITSGHALRILVMDVHHNGCTOMF	660
Db	601	GAAYVRPBGHNAEDDAACGCFEPNSVVAANHAQITSGHALRILVMDVHHNGCTOMF	660
QY	661	EDDPFVLVSLHRYDHGFPPMGDGAISOIGRAAGFTVNVANNGRMADADVLAMH	720
Db	661	EDDPFVLVSLHRYDHGFPPMGDGAISOIGRAAGFTVNVANNGRMADADVLAMH	720
QY	721	RLVLPRIAEFNPBELVYVACFDAAAGDVLGGCOVSPREYAHILTHILMLASGRILLLEG	780
Db	721	RLVLPRIAEFNPBELVYVACFDAAAGDVLGGCOVSPREYAHILTHILMLASGRILLLEG	780
QY	781	GYNLTSISESMAACTRSLILGDPPLTLPRPLSGALASITETIOVHHRRYRSLVMKVE	840
Db	781	GYNLTSISESMAACTRSLILGDPPLTLPRPLSGALASITETIOVHHRRYRSLVMKVE	840
QY	841	DREGSSSKLYTKKAPOPAKPRLAERMTTRKKYVLEAGMGAVTSASFEESTPGQTNSET	900
Db	841	DREGSSSKLYTKKAPOPAKPRLAERMTTRKKYVLEAGMGAVTSASFEESTPGQTNSET	900
QY	901	AVVALTOQPSSEAAATGATLAQITISEAIIIGAMIGQTTSEAVAGCATPDQTTSEETVGA	960
Db	901	AVVALTOQPSSEAAATGATLAQITISEAIIIGAMIGQTTSEAVAGCATPDQTTSEETVGA	960
QY	961	ILDDTTSEDAVALGATLGOTTISEAVVGAATLAQITISEAMEGATLDQTTSEAPGCTELIQ	1020
Db	961	ILDDTTSEDAVALGATLGOTTISEAVVGAATLAQITISEAMEGATLDQTTSEAPGCTELIQ	1020
QY	1021	TPPLASSPDHQPSPSPVQGTTPQISPLTIGSLTLEIGSISQASASQAPGEBNLLGEA	1080
Db	1021	TPPLASSPDHQPSPSPVQGTTPQISPLTIGSLTLEIGSISQASASQAPGEBNLLGEA	1080
QY	1081	AGGQDMADSMIQQSRGLTDQAIYYAATPLPWCHELVAVCPIPAAGLDVTYOPCDDCGTIO	1140
Db	1081	AGGQDMADSMIQQSRGLTDQAIYYAATPLPWCHELVAVCPIPAAGLDVTYOPCDDCGTIO	1140
QY	1141	ENMWCLSCYOYCGRYINGHMLDHGNSGHPVLVSYIDL\$AMCTYCOAYVHQAOLLEOVKN	1200

DB 1141 ENMWLSTCYQYCGXINCHMLOHNGNSGHPVLTITDLSAMCTYCOATVHQAALDPVN 1200
OY 1201 IAHQNKFGEDMPHP 1215
DB 1201 IAHQNKFGEDMPHP 1215

RESULT 3
AAB95640
ID AAB95640 standard; Protein; 817 AA.

AC AAB95640;
DT 26-JUN-2001 (first entry)
DE Human protein sequence SEQ ID NO:18380.
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-0116126.
XX 29-JUL-1999; 99JP-0248036.
XX 27-AUG-1999; 99JP-0300253.
XX 11-JAN-2000; 2000JP-0118776.
XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

DR WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

Claim 8; SEQ ID 18380; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 817 AA;

Query Match 62.98; Score 4022; DB 22; Length 817;
Best Local Similarity 99.38; Pred. No. 3.8e-312;
Matches 758; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MSTGQDSTTTTTRORSRONFQSPDSSVSKRIKKGAVPRSIPNLAEVKKKKMKKLG 60
DB 1 MSTGQDSTTTTTRORSRONFQSPDSSVSKRIKKGAVPRSIPNLAEVKKKKMKKLG 60
OY 61 QAMEEDLIVGLQGMNDLNEALAGTGLVLEQOLNEFHCLMDSPFGPBRHLAIKQOLI 120
DB 61 QAMEEDLIVGLQGMNDLNEALAGTGLVLEQOLNEFHCLMDSPFGPBRHLAIKQOLI 120
OY 121 QEGILDRCVSFQARFAKEKELMIVHSLEYIDMETTOYANMGEIRVLADYDVSYLHPNS 180
DB 121 QEGILDRCVSFQARFAKEKELMIVHSLEYIDMETTOYANMGEIRVLADYDVSYLHPNS 180
OY 181 YSCACLASGSVLRVAVLGAELIRNGMALTIRPGHHAQHSIMDGYCFNHVAARYAQO 240
DB 181 YSCACLASGSVLRVAVLGAELIRNGMALTIRPGHHAQHSIMDGYCFNHVAARYAQO 240
OY 241 KHRIRRVLIYDMDVHHGQGTQFTFDQPSVLYFSIHRYEQRFPHLKASNMSTGFGQG 300
DB 241 KHRIRRVLIYDMDVHHGQGTQFTFDQPSVLYFSIHRYEQRFPHLKASNMSTGFGQG 300
OY 301 QGYTIVPMNOVMGRADYIAAFILHLLPVALFQOLVYVAGFALQGDPRGEMATP 360
DB 301 QGYTIVPMNOVMGRADYIAAFILHLLPVALFQOLVYVAGFALQGDPRGEMATP 360
OY 361 AGPAQLTHLLMGLAGKLLILEGYNLRALAGVSASLTLLGDPCEMLSPGAPCRSA 420
DB 361 AGPAQLTHLLMGLAGKLLILEGYNLRALAGVSASLTLLGDPCEMLSPGAPCRSA 420
OY 421 QASVSCALEALPEFWEVLVSTETVERDNNEEDNVESEEGPEWEPVILTWVLIQSR 480
DB 421 QASVSCALEALPEFWEVLVSTETVERDNNEEDNVESEEGPEWEPVILTWVLIQSR 480
OY 481 TGLVYQONNMNHNLDSSHPEVPORTLRMCLEELGLNGRCUTLTPRRTAEELTCH 540
DB 481 TGLVYQONNMNHNLDSSHPEVPORTLRMCLEELGLNGRCUTLTPRRTAEELTCH 540
OY 541 SAEYVGLHRTATEMKTRRELHRESSNEDSIYICSTFCAQLATGAACRLVEAVLSGEVLN 600
DB 541 SAEYVGLHRTATEMKTRRELHRESSNEDSIYICSTFCAQLATGAACRLVEAVLSGEVLN 600
OY 601 GAAVVRPFGHHAQDAACGCFPNVSAVAARHAQTISGHALRILIVMDVHHNGTQHM 660
DB 601 GAAVVRPFGHHAQDAACGCFPNVSAVAARHAQTISGHALRILIVMDVHHNGTQHM 660
OY 661 EDDPSVLYVSLAHYDGTFFPMGDEGASSQIGRAAGCFVNVAMNGBRMGDADYLAAMH 720
DB 661 EDDPSVLYVSLAHYDGTFFPMGDEGASSQIGRAAGCFVNVAMNGBRMGDADYLAAMH 720
OY 721 RLVLPTAYEPNELVIVSAGFDAAAGDPLGCGVSPGVAHLT 763
DB 721 RLVLPTAYEPNELVIVSAGFDAAAGDPLGCGVSPGVAHLT 763

RESULT 4
AAB93058
ID AAB93058 standard; Protein; 726 AA.

AC AAB93058;
DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:11864.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

PN EP1074617-A2.

cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116176-AB130511), expressed DNA sequences (AB101840-AB116175) and the encoded proteins (AB17737-AB172072).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 883 AA;

Query Match 28.3%; Score 1810; DB 22; Length 883;
 Best Local Similarity 46.7%; Pred. No. 2.7e-135;

Matches 371; Conservative 135; Mismatches 237; Indels 52; Gaps 17;

86 TGLVDEQNEFCLMDSPFEPERLHAKEQLDGLDRCVSGFARPEKEELVH 145
 31 TALIYDESMOHCCLMDKEHECPERTVRLERCLNTERLELPSRSATDELRLH 90
 146 SLEFYD-LMETTOYANEGELRVADTYDYLHPNSTSCAGSLVRLVDVLAIEIR 204
 91 TEEHEERLKETSGIRDERMEELSSRYDSIYIHPSTFELSLASGSIYELVDHLVAGKQ 150
 205 NGMAIIRPPGHAHSHLMDGYCMFNHVAAYARAOQKHRIIRVLIYDMVDVHGGQTFE 264
 151 NGMAIIRPPGHAHMAKAEYNGICEFNVALATOHALDVHKLQRLITLDYVHGGQTFE 210
 265 DDDPSVLYPSIHRYEGRFPHLKASNMSTTGFQGGQGYTINPMNOVGKRDADYIAFL 324
 211 YMDPRVYVESIHREHGFSPHPLHESDYHAISGAGGVNFNPLNATGMTNDYALAFQ 270
 325 HTLLPVALEFOPOLVVAAGFDALODPKGEMATPAGRQTLHLMGLAGKLLISLEG 384
 271 QLLLPVALEFOPELIIVSAGYDALGCPREGEVETPACYPHLLNPLRLADAVAVYLEG 330
 385 GYNLRALAGVSASLTLLGDPC-PMLESPPGAP-CSSAOSVSCALELEPFEVL-VRS 441
 331 GTCIDSLAGCALTLRLSLGDCPPRLVEYTPRLRAELAOALLSC-IAYHPRHRCLOLQ 389
 442 T-----ETVRDNKED-NVESEEDGPMPPV-----LP1-----WT-----WVPL 477
 390 TDCVELADORDK-EEDLHTVLRHWIGSP--PPMDRYPTROTALPRLPEKLTSAARLOVL 446
 478 GSRFTG-----YDDNMAMHCHLMDSHNEPVQRIIRKCRLEELGLAGRCYLTLP 528
 447 RAETKLSVPSFYCYAYDAOMLHACMLNDTGHNEQPSRLOHIMKMDVGLKQOMOLSP 506
 529 RATEAEELTCHSAEYVGHILRATERKKTREHRESSNFDSIYCPSFACOLATGACR 588
 507 RAATIDEVCLARTRAHVNTVRLRGREPKELHDAAGIYNSVYLHPRTFCATLAAGLVQ 566
 589 LVEAVLSEGLNGAAYVRRPGHNAEDAACGFCFNSVANVAARHAOTISGHAL-RILIVD 647
 567 AVDSVLRGSRSGICNVRRPGHNAEDQHPHGFICFNNVLAAGYA--IRFGLERLVLD 624
 648 WYVHNGNGQHMFEDDPSTLYVSLHRYDCTFFPMGDEGASSOIGRAAGTGFVNVAWG 707
 625 WYVHNGNGQHMFESNPKVLYISLHRYEHSFEPKPDGDFDVVAGAGGFVNVTIPWK 684
 708 PRMGADADYLAAMHRLVLTAYEFNPETLYVSAGFDDAARGLGGCOVPSAHLHLHM 767
 685 KMGMDLEVALAFOLIMPIAYEFNPOLVLSAGFDALGDPGLGCKVYLAEGYMLTHMS 744
 768 GLASGRITLLLEGVNLTSISSMACTRSLLGDDPP-----LTLTPRP--LSGALAS 819
 745 ALASGRITVCLLEGVNVISYAMTMCSTLTGLDPPVPTQLGATFALOKPPTVAFQSCVES 804
 820 ITETIQVHRRYRSL 834
 805 LOOCLOVOGNHWRSL 819

RESULT 6

AAU00244
 ID AAU00244 standard; Protein; 363 AA.
 XX
 AC AAU00244;
 XX
 DT 18-MAY-2001 (first entry)
 XX
 DE Human histone deacetylase 6, HDAC6.
 XX
 KW Histone deacetylase-like protein; HDLP; inhibitor; crystal; cancer;
 KM three dimensional structure; protein coordinate data; HDAC6;
 KW rational drug design; histone deacetylase.
 OS Homo sapiens.
 XX
 PN WO200118045-A1.
 XX
 PD 15-MAR-2001.
 XX
 PE 08-SEP-2000; 2000WO-US24700.
 XX
 PR 08-SEP-1999; 99US-0152753.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Pavletich N, Finnin M, Donigian J, Richon V, Rifkind RA, Marks PA;
 PI Breslow R;
 DR WPL; 2001-226741/23.
 XX
 PT A new 4 Angstrom crystal structure of an enzyme comprising deacetylase
 PT activity, where the enzyme possesses a conserved alpha/beta structure
 PT used for screening and identifying potential deacetylase inhibitor
 PT compounds -
 XX
 PS Disclosure; Fig 2; 329pp; English.
 XX
 CC The sequence represents the amino acid sequence of histone deacetylase 6
 CC (HDAC6) used to identify the sequence of histone deacetylase-like protein
 CC (HDLP) used in the course of the invention. The HDLP sequence was used to
 CC identify a potential deacetylase inhibitor compound comprising: (a) using
 CC a three dimensional (3D) structure of HDLP as defined by the atomic
 CC coordinates fully defined in the specification; (b) employing the 3D
 CC structure to design or select the potential inhibitor. A crystal of the
 CC enzyme, and its mutants, such as a Cys75Ser/Cys77Ser double mutant of
 CC HDLP, and a Tyr297Phe active site mutant of HDLP, comprising deacetylase
 CC activity was determined where the crystal diffracts x-rays for the
 CC determination of the atomic coordinates of the enzyme to a resolution
 CC greater than 4 Angstrom. The crystal is used for screening for a novel
 CC drug comprising: (a) selecting an inhibitor by performing rational drug
 CC design with the 3D structure determined from the crystal; (b) contacting
 CC the inhibitor with the ligand binding domain of the crystal; and (c)
 CC detecting the binding potential of the inhibitor for the ligand binding
 CC domain, where the novel drug is selected based on its having a greater
 CC affinity for the ligand binding domain than for the known drug. The drug
 CC may be useful for inhibition of cell growth in the treatment of cancer.
 XX
 SQ Sequence 363 AA;

Query Match 27.3%; Score 1749.5; DB 22; Length 363;
 Best Local Similarity 89.4%; Pred. No. 4.5e-131;
 Matches 363; Conservative 0; Mismatches 0; Indels 43; Gaps 14;

83 LAGTGLVLDQLENEFCLMDSPFEPERLHAKEQLDGLDRCVSGFARPEKEELM 142
 1 LAGTGLVLDQLENEF-----PPEGERLHAKEQLDGLDRCVSGFARPEKEELM 52
 143 LVHSLFYDLMETTOYANEGELRVADTYDYLHPNSTSCAGSLVRLVDVLAIEIR 202
 53 LVHSLFYDLMETTOYANEGE-RVADTYDYLHPNSTSCAGSLVRLVDVLAIEIR 111
 203 IRNGMAIIRPPGHAHSHLMDGYCMFNHVAAYARAOQKHRIIRVLIYDMVDVHGGQTF 262

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DB 112 -----AIIIPPHHAAHSLMDGTICMHNVAARVIAQKH-IRRLVIVMDVHHGGOTF 165
OY 263 TFDODPSVLYFSIHREYQGRFMPHLKASNMSTGFGOGGYTINVPMNOVGMADAYIA 322
DB 166 TFDODPSVLYFSIHREYQGRF-PHLKAS-WSTTGFGOGGYTINVPMNOVGMADAYIA 222
OY 323 FLHVLPALEPQPOLVLAAGFDALQDPKGMMAATPAGFQJTHLMGLAGKILSL 382
DB 223 FLHVLPALEPQPOLVLAAGFDALQDPKGMMAATPAGFQJTHLMGLAGKILSL 282
OY 383 ECGYMRALAEVSAISHTLGDPCMLESPAPCSASAASVSCALEPEFVYVRS 442
DB 283 -GGYMRALAEVSAISHTLGDPCMLESP-GAPCSASAASV-----EPFWEIVLRST 334
OY 443 ETVERDNMEEDVNESEEGEPVPLPILTWPVLOSRTGLVYDQN 488
DB 335 ET-----EDNV-----EPVPLPILTW-LOSRGTGLVYDQN 363

RESULT 7
AAB42743
ID AAB42743 standard; Protein; 675 AA.
AC AAB42743;
XX
DT 08-FEB-2001 (first entry)
XX
XX Human ORF2507 polypeptide sequence SEQ ID NO:5014.
DE
XX
XX Human; open reading frame; ORF; detection; cytosolic; hepatotropic;
XX vulnerable; antiparionian; antiparionian; neutrotropic; neuroprotective;
XX anticonvulsant; osteopathic; antidiabetic; immunosuppressant; cardiant;
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
XX hypotensive; dermatological; immunosuppressive; antidiabetic;
XX antiviral; antibacterial; antifungal; antineoplastic; antihypertensive;
XX antineoplastic; gene therapy; cancer; proliferative disorder; hypertension;
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
XX cholesterol ester storage; systemic lupus erythematosus; infection;
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
XX thrombosis; cartilage damage; inflammatory disease; coagulation;
XX
XX Homo sapiens.
OS
XX MO200058473-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000MO-US08621.
XX
XX 31-MAR-1999; 99US-0127607.
XX 02-APR-1999; 99US-0127636.
XX 05-APR-1999; 99US-0127728.
XX 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
XX
XX MPI; 2000-602362/57.
XX
XX N-PSDB; AAC76952.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
XX useful for treating e.g. cancers, proliferative disorders,
XX neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 11; Page 4195-4196; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORF open reading frames 1 to 3161. The ORF
CC

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CC sequences have activities such as: cytostatic; hepatotropic; vulnerable;
CC antiparionian; antiparionian; neutrotropic; neuroprotective;
CC osteopathic; anticonvulsant; antidiabetic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antineoplastic; antineoplastic; antineoplastic; antineoplastic;
CC antineoplastic; antineoplastic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORF-associated disorder. The
CC nucleic acids can be used to express ORF proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, inflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX
XX Sequence 675 AA;
XX
XX Query Match 17.7%; Score 1132; DB 21; Length 675;
XX Best Local Similarity 36.6%; Pred. No. 2.7e-81;
XX Matches 290; Conservative 92; Mismatches 240; Indels 170; Gaps 22;
XX
OY 69 VGLQGMDELNEAFLAGTGLVDEQNEFICLMDSP-----EGPERLHAKEDLIQEG 124
DB 4 LGTGG-----DHGAMGTALVYHEDMTATLLMD--PECEIERPERLTAALDRKGL 56
OY 125 LRCVDFQARFAKEELIMVHSLYIDIMETTYOMNGELRVADTVSYLHNSYSCA 184
DB 57 EQGCLILASREASEEELGLVHSPDYSLVRETVYLGKEELQALSGCDALYHNSYSCA 116
OY 185 CLASGVLRVDAVLAETIRNGMAITIRPGHNAOSHIMDGYCMFNHVAARVIAQKHRI 244
DB 117 RLAAAGGLDLDVAVLTVGAONGDALVRPQHGOAANFCVFNNAIAAHAKOKHGL 176
OY 245 RRLVYDMVYHNGOQGFEDDOPSVLYEISIHREYQGRFMPHLKASNMSTGFGOGGYT 304
DB 177 HRLVYDMVYHNGOQGFEDDOPSVLYEISIHREYQGRFMPHLKASNMSTGFGOGGYT 236
OY 305 INVPMNOVGMADAYIAEFLHVLPALEPQPOLVLAAGFDALQDPKGMMAATPAGFA 364
DB 237 VNLPMNOVGMADAYIAEFLHVLPALEPQPOLVLAAGFDALQDPKGMMAATPAGFA 296
OY 365 QLTHLMGLAGKILSLBGGIVLRLALAEVSAISHTLGDPCMLESPAPCR-----SA 420
DB 297 HLTOLQVLAAGVCAVLEGGYHLESVCMTVOFTLLGDPAPPLSGPAPAPCORCEGSA 356
OY 421 QASVSCALALPEFVWLVRSFTVERDNMEEDVNESEEGEPVPLPILTWPVLOSRT 480
DB 357 LESIGARAAQAPHMSLQOQDYTA---VPMSPSSHPGRP--PPLD--GGPVKAA 408
OY 481 TGLVYDQNMNHNCLNDSHHPYORILRLMCRLEELIAGRCGLTLTPRPATB-AELLTC 539
DB 409 A-----SAPSSLDQPC-----LCRAPSVTAVALTT 435
OY 540 HSAETV-----GHLPAEKMKTR--ELHRSNFDISTYICPSPFACQALATGAA 586
DB 436 PDITVLPPDVITQESASALRETEAWARPHESLARBE-----ALTLGKL 480
OY 587 CRVLEAVLSGEVLNGAAYVRPGCHNAEDQACGFCFNSVAVYAAKQOTISGALRLIY 646
DB 481 IYLLGMDGQVNSGIAATPASAATAATD-----VAVRG--LSHQAORILCY 526
OY 647 DMDVHNGMGTOMFEDDPSVLYSLRYDHGTFFPMGDEGASQIGRAAGTGTVNVANM 706
DB 527 -----ALGQLRPPDLAHGSLWL 546
OY 707 GPRMGADADYLAAMH-----RLVLPPIAEFNPDELVVSAGFADARGDPL 749
DB 547 NIKREAAALSMFHVSTPLPVMTGTFGLSCITGLVPLAVGFGOPDVLVNLG-----PG 599

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DR N-PSDB; ABO73028.
 XX Novel histone deacetylase 9 polypeptide and polynucleotide encoding the
 PT polypeptides, useful for diagnosing conditions related to abnormal
 PT polypeptide activity e.g., cancer, atherosclerosis, psoriasis -
 XX
 PS
 XX Claim 1, Fig 2B; 103pp; English.
 CC The present invention describes histone deacetylase (HDAC) 9 proteins
 CC (1). (1) has cytostatic, antiproliferative, antiatherosclerotic and
 CC antiinflammatory activities, and can be used in gene therapy and as a
 CC normal transcription regulator. (1) can be used in the diagnosis of a
 CC condition associated with abnormal HDAC9 expression or activity in a
 CC human. Polynucleotides encoding (1) can be used for the diagnosis of a
 CC condition associated with abnormal regulation of gene expression which
 CC includes, abnormal cell proliferation, cancer, atherosclerosis,
 CC inflammatory bowel disease, host inflammatory or immune response, or
 CC psoriasis in humans which comprises detecting abnormal transcription of
 CC messenger RNA transcribed from the natural endogenous human gene encoding
 CC (1) an appropriate tissue or cell from a human, where the abnormal
 CC transcription is diagnostic of the condition. The present sequence
 CC represents human HDAC9 from the present invention.
 CC
 XX
 XX Sequence 673 AA:

Query Match 17.6%; Score 1125; DB 23; Length 673;
 Best Local Similarity 37.2%; Pred. No. 9, 8e-81;
 Matches 283; Conservative 89; Mismatches 225; Indels 164; Gaps 20;

QY 85 GTGVLADLNENHCLMDDSPF---EGPERLAIKEOLIOGLDRCVSFOARFAEKEE 140
 DB 2 GTALVYHEMDMTRLLMD--PECEIERPERLTAALDRKORLEQCLRLSARESEEE 59
 QY 141 LMLVHSLEYIDMETTYQYNEGELRYLADYDSVYLHPNSYSCACIASSGVRLYDAVLG 200
 DB 60 LGIVHSPEYSLVRETYQYNGKELOALSGQFDALYFHFSTFCARLAAGAGLDVAVLT 119
 QY 201 AEIRNGMALIRPGHHAQSLMDGYCMFNHVAARVAAQOKRIRRVLYVDMVNHGOGT 260
 DB 120 GAVONGIALVRRPGHGHGQRAAANGFCVFNNVAIAAHAQKHRLHRLYVDMVNHGOGI 179
 QY 261 QFTFDODPSVLYFSIHRYEGGRFPHILKASNMSTGFGGOGYTTINVPNGVGMADYI 320
 DB 180 QYLFEDDPSVLYFSIHRYEGGRFPHILKASNMSTGFGGOGYTTINVPNGVGMADYI 239
 QY 321 AAFHLVLLPALIEPOPVLVVAAGFDALQDGRKGEAATPAFAOTLHLLMGLAGKLT 380
 DB 240 AAFHLVLLPALIEPOPVLVVAAGFDALQDGRKGEAATPAFAOTLHLLMGLAGKLT 299
 QY 381 SLEGGYNRLAEGVSASLHTLIDPCPYLESPPAPCR---SAQASVSCALEALEPFE 436
 DB 300 VLEGGYHLESLEASVCMYVOTLLGDPAPPLSGPMAPCCQCEBSALESTIOSARAAQAPHWK 359
 QY 437 VLVSTETVERDNMEEDNVESEEGPWEPPVLPITLTPVLSRTGLVYDQMMNHNCML 496
 DB 360 SLQGDQDTA---VMSPSSSHPEGRP--PILLP--GGPVCKAAA----- 396
 QY 497 DSHHEPQRIIRIKRLEELGLAGRCITLTPRPATE--AELLTCHSAEYV----- 545
 DB 397 ---SAPSSILDDQPC-----ICPAPSVRTAVALTTPDITLVLPPVIOQEA 438
 QY 546 GHILATEMKTR---ELHRESNFDISYICPSTFACQALATGACRLVAVVSGEVLNKA 602
 DB 439 SALRETEAAMAPHESLARE---ATLALGLKLYLLDGMIDGOVNSGI 483
 QY 603 AVVRRPGHHAQDAGCFENSVAAARNAQTIIGHALRLITVDMVNHGOGTQMFED 662
 DB 484 AATPSAAATLTD-----VAVRRG--LSHGAKRLCY----- 513
 QY 663 DPSVLYVSLHRYDGTFFPMDEGASQSIGRAAGTGFTVNVAMNGPRMGDDADYLAAMH-- 720
 DB 514 -----ALGQIDRPPDLAHDRSILMLNRGEAAALASMEFHS 549

QY 721 -----RLVLPYAEFNPETLYSAGFPAARGDPLGGQVPEGYAHLTHL 765
 DB 550 TPLPMTGGFLSCITIGLIVPLAYGFQDPLVALVG-----PEHGLO--GPHA--ALLAAM 600
 QY 766 IMGLASGRITLLEGGVNLISSESMACRYSLGDPPPL 806
 DB 601 LRGLAGRYALALE-----NSTPQLAGILARVINGENRPPSL 637

RESULT 11
 AAE22854
 ID AAE22854 standard; Protein; 673 AA.
 AC AAE22854;
 XX
 XX 21-AUG-2002 (first entry)
 DT
 XX
 XX Human histone deacetylase protein.
 DE
 XX
 XX Human; histone deacetylase; therapy; cancer; bait protein; cytostatic;
 KW enzyme.
 KW
 XX Homo sapiens.
 OS
 XX
 XX MO200230970-A2.
 PN
 XX 18-APR-2002.
 PD
 XX
 XX 11-OCT-2001; 2001MO-EP11759.
 PF
 PR 13-OCT-2000; 2000US-239928P.
 XX
 XX (FARB) BAYER AG.
 PA
 XX
 XX Zhu Z;
 PI
 XX
 XX WPI: 2002-416859/44.
 DR N-PSDB; AAD36979.
 DR

PT New human histone deacetylase polypeptide useful for identifying
 PT modulating agents that can be used for treating diseases such as cancer
 PS Claim 25; Fig 2; 116pp; English.

CC The present invention relates to novel histone deacetylase proteins and
 CC polynucleotides encoding them. Sequences of the invention are useful for
 CC identifying modulating agents that are used for preventing, ameliorating,
 CC treating or correcting dysfunctions or diseases such as cancer. They can
 CC also be used to screen for human histone deacetylase activators and
 CC inhibitors. They are useful for generating antibodies and can be used as
 CC bait proteins in two-hybrid assay or three-hybrid assay. The present
 CC sequence is human histone deacetylase protein.
 CC
 XX
 XX Sequence 673 AA:

Query Match 17.6%; Score 1125; DB 23; Length 673;
 Best Local Similarity 37.2%; Pred. No. 9, 8e-81;
 Matches 283; Conservative 89; Mismatches 225; Indels 164; Gaps 20;

QY 85 GTGVLADLNENHCLMDDSPF---EGPERLAIKEOLIOGLDRCVSFOARFAEKEE 140
 DB 2 GTALVYHEMDMTRLLMD--PECEIERPERLTAALDRKORLEQCLRLSARESEEE 59
 QY 141 LMLVHSLEYIDMETTYQYNEGELRYLADYDSVYLHPNSYSCACIASSGVRLYDAVLG 200
 DB 60 LGIVHSPEYSLVRETYQYNGKELOALSGQFDALYFHFSTFCARLAAGAGLDVAVLT 119
 QY 201 AEIRNGMALIRPGHHAQSLMDGYCMFNHVAARVAAQOKRIRRVLYVDMVNHGOGT 260
 DB 120 GAVONGIALVRRPGHGHGQRAAANGFCVFNNVAIAAHAQKHRLHRLYVDMVNHGOGI 179
 QY 261 QFTFDODPSVLYFSIHRYEGGRFPHILKASNMSTGFGGOGYTTINVPNGVGMADYI 320

OY 717 AAMHRLVPIAYEFNPETLVASGFDANGDPLGGCQ 753
Db 539 SCITGLVPLAYGFDPDLVALG-----PQHGR 568
RESULT 13
AAU23410
ID AAU23410 standard; Protein; 330 AA.
AC AAU23410;
XX 18-DEC-2001 (first entry)
DE Novel human enzyme polypeptide #496.
XX
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KM ligase; hyperproliferative disorder; immunodeficiency disorder;
KM autoimmune disorder; neurological disorder; metabolic disorder;
KM inflammatory disorder; cardiovascular disorder; reproductive disorder;
KM blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KM neoplastic; anticoagulant.
XX Homo sapiens.
OS WO200155301-A2.
PN 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01239.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205315.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246539.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465566/50.

N-PSDB; AAS41280.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases

Claim 11; SEQ ID No 1406; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. hemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polynucleotides of the invention can also be used in gene therapy. AAD22915-AAD23814 represent the novel human enzyme polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 330 AA;

Query Match 14.0%; Score 895; DB 22; Length 330;
 Best Local Similarity 55.6%; Pred. No. 7; 6e-63;
 Matches 163; Conservative 56; Mismatches 74; Indels 0; Gaps 0;

DB 107 EGPRLHAIKEOLIOGLDRCVSPQAFARKEELMLVHSLEYIDIMETQYNNEGELRY 166
 | | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : : | |
 35 EPPERLTAIDRLRQGLRQRCRLSARKESEELGVHSPEVSVLVRETVQVGLKELXA 94
 167 IADTVDSVYLHPNSYSCACIAGSVLRYDAVLAIEIRNGMATIRPGHHAQSLMDGYC 226
 | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | |
 DB 95 LSGQDAIFYHPSSTFCARLAAGAGQLVDVLTGAIVONGIALVRRPGHHGQAAANGFC 154
 227 MNNHVAARVAAQOKHRIKRVILVMDVHHGSGTQTFPDPSVLYFSIHRYEGGRFMPH 286
 | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | |
 DB 155 VFNHYIAAARAKORHGRILVVDVHHGQIQVLFEDDPSVLYFSHRYEGGRFMP 214

QY 287 LKASNMSTTGFQGGQGITINVPNOVGMNDADYIAFLHVLVPALEFQPOLVLAAGFD 346
 | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | |
 DB 215 LRESADAVAGRGQGGIGFTVNNLPWNOVGMNDYVAAFLLHLLPLAXXFPPELVYSAGD 274
 QY 347 ALQDPKGEAMATPAGFAQLTHLLNGLAGCKLILSEGGYNLRALAEVGSASL 399
 | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | |
 DB 275 SAIGDPGOMQATPECFALHQLQLVLAGRGVCAVLEGXHLSELAEXYKMTV 327

RESULT 14

AAB49957 standard; Protein; 967 AA.

AAB49957;

08-MAR-2001 (first entry)

Human histone deacetylase HDAC-4.

Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

gene therapy.

Homo sapiens.

WO200071703-A2.

30-NOV-2000.

03-MAY-2000; 2000WO-IB01252.

03-MAY-1999; 99US-0132287.

(METH-) METHYLENE INC.

MacLeod AR, Li Z, Besterman JM;

WPI; 2001-016407/02.

N-PSDB; AAC89557.

Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms of neoplasia, or for inhibiting neoplastic cell growth in an animal -

Disclosure; Page 56-59; 125pp; English.

The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These inhibitors may be antisense strands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and for identifying which histone deacetylase is involved in a neoplasia.

Sequence 967 AA;

Query Match 12.6%; Score 805.5; DB 22; Length 967;
 Best Local Similarity 46.0%; Pred. No. 6e-55;
 Matches 185; Conservative 54; Mismatches 118; Indels 45; Gaps 12;

QY 465 EPPVLPITLTPVLDQSRGLVYDQNMNHN-CNLW-DSHHPEVPORTLRIMCRLEELGLGR 522
 | | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : : | |
 DB 528 EPPKRPFT-----TGLVYDITMLNHOCTGSSSSHPHAGRIQSTWSRLQETGLNGK 580
 QY 523 CLTLPPTATEAEILLTCHSAEYVGHRLATEKMKTRLEHRE-----SSNF----- 566
 | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | |
 DB 581 CEQJRGKATLEELQTVHSEHNT-LTGTNPINQKXDKSLGSLASVFRILPCGGVGV 639
 QY 567 --DSIYICPSTFCAQATGACRLVAVLSGEVLNGAAYVRPGHHAEDADAGCFEPN 624
 | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | |
 DB 640 DSDITMNEVNSAGARLAVGCVVELYKVAITGELKNGFAVAVRPGHHAESTPMGFCYFN 699
 | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | |
 QY 625 SVAVAAARHAC---TISGHALRIILVDMVHHGNGTQIMFEDDPSVLYVSLHRYDHGTFPP 681

```

Db      700 SVAFAAKLLDQRLSVS-----KILIVDMVDVHNGNGTQQAFTSPDSVLYMSLHRRDDGNFFP 755
      682 MGDEGASSQIGRAAGTGTNNVAMNG---PRMGDADYLAAMHRLVPIAYEFNPELVLS 738
      756 --GSGAPDEVGTGPGVGFNNMAFTGGLDPPMDAEYLAAFRTVYMPFIASEFAPDVVLVS 813
QY      739 AGFDAARG--DPLGGCVSPREGYAHNLHLMGLASGRILILEGGYNLTSISSEMAACTR 796
      814 SGPDAVEGHPTPLGGYNLSARCFGYLTKQLMGLAGGRIVALEGGHDLTAICDASACVVS 873
QY      797 SLUG---DPPLLTLPRPLSGALASITETIOVRRYRSLSR 835
      874 ALLGNELDPLPEKVLQQRPNANNAVRSMEKWEIHSKTRCLO 915
Db
RESULT 15
AAU99659
ID      AAU99659 standard; Protein; 967 AA.
XX
AC      AAU99659;
XX
DT      07-OCT-2002 (first entry)
XX
DE      Human Histone deacetylase isoform 4.
XX
KW      Human; histone deacetylase; HDAC-4; cancer; cytostatic;
KW      antisense; tumour suppressor; cell proliferation; tumour;
KW      programmed cell death; necrotic cell death.
XX
OS      Homo sapiens.
XX
FH      key Location/Qualifiers
FT      Misc-difference 72 /note= "Encoded by CCG"
FT      Misc-difference 78 /note= "Encoded by ACT"
FT      Misc-difference 80..81 /note= "Encoded by AGAGAC"
FT      Misc-difference 135 /note= "Encoded by TCA"
FT      Misc-difference 194..196 /note= "Encoded by GCGTGGAGG"
FT      Misc-difference 318 /note= "Encoded by GTA"
FT      Misc-difference 574 /note= "Encoded by AAG"
FT      Misc-difference 701 /note= "Encoded by GCG"
FT      Misc-difference 775 /note= "Encoded by ACG"
FT      Misc-difference 812 /note= "Encoded by GTC"
FT      Misc-difference 948 /note= "Encoded by GAC"
FT      /note= "Encoded by GAC"
XX
PN      US2002061860-A1.
XX
PD      23-MAY-2002.
XX
PF      06-AUG-2001; 2001US-0817913.
XX
PR      24-MAR-2000; 2000US-192157P.
XX
PA      (LIZZ/) LI Z.
PA      (BONF/) BONFILS C.
PA      (BEST/) BESTERMAN J.
XX
PI      LI Z, Bonfils C, Besterman J;
XX
WPI; 2002-507650/54.
DR      N-PSDB; ABR87718.
XX

```

```

PT      Agent that specifically inhibits an isoform of histone deacetylase,
PT      useful for treating cancer and other cell proliferative diseases,
PT      preferably comprises an antisense oligonucleotide
XX
PS      Disclosure; Fig 4A; 60pp; English.
XX
CC      The invention relates to an agent that inhibits an isoform of histone
CC      deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an
CC      antisense oligonucleotide. Also included are inhibiting an HDAC isoform
CC      in a cell by treatment with the agent, identifying an HDAC isoform that
CC      is required for induction of cell proliferation or differentiation and
CC      inhibiting cell proliferation by treatment with two antisense
CC      oligonucleotides or small molecules that inhibit a specific HDAC
CC      isoform, or antisense oligonucleotide or small molecules that inhibit
CC      DNA methyltransferase. The agent therefore acts as a tumour suppressor.
CC      The agents are used to treat diseases of cell proliferation and
CC      differentiation (e.g. cancer and tumours), by inducing growth retardation,
CC      growth arrest or programmed/necrotic cell death, specifically neoplastic
CC      cell proliferation in humans. The agents are selective for particular
CC      isoforms, compared to known inhibitors which are not selective.
CC      The present sequence represents the HDAC-4 isoform.
XX
SQ      Sequence 967 AA;
XX
Query Match 12.5%; Score 801.5; DB 23; Length 967;
Best Local Similarity 45.8%; Pred. No. 1.2e-54;
Matches 184; Conservative 54; Mismatches 119; Indels 45; Gaps 12;
QY      465 EPPVPLITWPIVLSRTGLVYDQNMNHN-CNLW-DSHHPVOPRILRMCRLEELAGLR 522
      528 EPPTKPRFT-----IGLYVDLMLKHQCTCGSSSHPRHAGNIGQISWISLQETGLNGK 580
QY      523 CLTLTPRPATEALLTCHSAEYVGHRLATEKMKTRLEHRE-----GSNF----- 566
      581 CECIRGKATLEIELQTVHSEAHN-TLXTNPLNRQKLDKSLASLSEFVRLPCGGVGV 639
QY      567 --DSITYCPSTFACAOATGACRLVAVLSGEVLNGAAVVRPGRHAEODAAAGFCPEN 624
      640 DSPTIMNEVHSAGARLAVGVVELVFKVATGELKNCFAYVVRPGRHAEESTPMGFCYFN 699
QY      625 SVAFAARHAQ---TISGHALRILIVDMVDVHNGNGTQQAFTSPDSVLYMSLHRYDHGTFPP 681
      700 SVAFAAKLLDQRLSVS-----KILIVDMVDVHNGNGTQQAFTSPDSVLYMSLHRYDGNFFP 755
Db      739 AGFDAARG--DPLGGCVSPREGYAHNLHLMGLASGRILILEGGYNLTSISSEMAACTR 796
      814 SGPDAVEGHPTPLGGYNLSARCFGYLTKQLMGLAGGRIVALEGGHDLTAICDASACVVS 873
QY      797 SLUG---DPPLLTLPRPLSGALASITETIOVRRYRSLSR 835
      874 ALLGNELDPLPEKVLQQRPNANNAVRSMEKWEIHSKTRCLO 915
Db

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Search completed: June 6, 2003, 14:59:58
 Job time : 58 secs

727 AEFNPPELVLSAGGDAARGDP.LGGCQVSPEEYAHITHTLMGLASGR--ITLLEGVYL 784
 | : : : : | | | | : : : : | : : : : | | | | :
 Db 236 VEEKPKIVISAGDGFEGDGLTTLRLTESFSY-----AGATLNKYPPLAF.LLEGYGV 290

```

RESULT 2
US-09-712-266-80
Sequence 80, Application US/09712266
Patent No. 6333158
GENERAL INFORMATION:
APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshimi
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MIKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoskin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408BCT
CURRENT APPLICATION NUMBER: US/09/712,266
PRIORITY FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 335
TYPE: PRF
ORGANISM: Pyrococcus furiosus
US-09-712-266-80

```

[illegible]

RESULT 3
US-09-282-305-8
Sequence 8, Application US/09282305
Patent No. 6287843
GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maltize HisTone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305

```

: CURRENT FILING DATE: 1999-03-31
: PRIOR APPLICATION NUMBER: 60/080,565
: PRIOR FILING DATE: 1999-04-03
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEC ID NO 8
: LENGTH: 517
: TYPE: PRN
: ORGANISM: Zea mays
US-09-282-305-8

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	Query Match	4.6%;	Score 292;	DB 4;	Length 517;	
	Best Local Similarity	26.7%;	Pred. No. 8.9e-17;			
	Matches	89;	Conservative	61;	Mismatches 145;	Indels 38; Gaps 11
QY	485	YDQNMNMHCLMDSHNEPVRQILRLIMCRLELISAGRCILTLTPRPATAEALITCSAAY	544			
		Y D P P V G N Y - Y G G G H P M K P H R I M T H S I L A R Y G L L M Q Y R P R A P A R D R D L C R F R H A D Y				
Db	29	Y D P P V G N Y - Y G G G H P M K P H R I M T H S I L A R Y G L L M Q Y R P R A P A R D R D L C R F R H A D Y	86			
QY	545	VGHRA-----TEKKKTRELAR-----SSNFDSIYICSTYACQALATGAACRL-----V	590			
		V H G H R A - - - - - T E K K K T R E L A R - - - - - S S N F D S I Y I C S T Y A C Q A L A T G A A C R L - - - - - V				
Db	87	INFLRSTPPEOQDQILRLKRFNVGEOCPVFDGIYSPFOYTAGA--SVGGAVKLNHGDI	144			
QY	591	EAVLSGEVINGAAVVRPRGNHAEDDAAGCGCFEFSVAANAHAQITISHALRIILVDMDY	650			
		E A V L S G E V I N G A A V V R P R G N H A E D D A A G C G C F E F S V A A N A H A Q I T I S H A L R I I L V D M D Y				
Db	145	AIMNSGVL-----HHAKKCEASGFEYVDIVATILE--LKNHREVLVDIDI	190			
		A I M N S G V L - - - - - H H A K K C E A S G F E Y V D I V A T I L E - - L K N H R E V L V D I D I				
QY	651	HHGNGTGHMEEDDESVLYVSLIHRDHTGTFEPMGDEGASASQGRAAGTFYVNAVANGPRM	710			
		H H G N G T G H M E E D D E S V L Y V S L I H R D H T G T F E P M G D E G A S A S Q G R A A G T F Y V N A V A N G P R M				
Db	191	HHGGGVGEALYTTDRVMTVSFHKF--GDYFP--GTGDRIDRGHSKXKRYISLWPLD--DGI	245			
		H H G G G V G E A L Y T T D R V M T V S F H K F - - G D Y F P - - G T G D R I D R G H S K X K R Y I S L W P L D - - D G I				
QY	711	GDADYLAAMHRLVPLIAYEENPELIVVSAGFDAARGDPLGGGQVSPEGYAHLTTHLMGIA	770			
		G D A D Y L A A M H R L V P L I A Y E E N P E L I V V S A G F D A A R G D P L G G G Q V S P E G Y A H L T T H L M G I A				
Db	246	DDESYOSLFPRIMKVAEVEFRGAVVULQCGADSLSGDRLCGFNLSIKGHACACVYMRSF--	304			
		D D E S Y O S L F P R I M K V A E V E F R G A V V U L Q C G A D S L S G D R L C G F N L S I K G H A C A C V Y M R S F - -				
QY	771	SGRIILLGEGYNLTSSMAACTRSLDGRP	803			
		S G R I I L L G E G Y N L T S S M A A C T R S L D G R P				
Db	305	NPELLLEGGGYYIRNVARCWCYETGVALGQEP	337			

```

RESULT 4
US-09-282-305-6
; Sequence 6' Application US/09282305
; Patent NO. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Matzke Histone Deacetylases And Their Use
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 439
; TYPE: PR1
; ORGANISM: Zea mays
; US-09-282-305-6

```

Query Match	Similarity	Score	290.57	DB 4	Length	439	
Best Local	Similarity	27.38	Pred. No.	9e-17			
Matches	92	Conservative	61	Mismatches	153	Indels	31
							Gaps
							13
QY	485	YDQNMNHCMLQMSHPPEVORILIRKICRLEELGLARCLLTTPRPAPAEALLCHSMEY	544				
Db	28	YDAEYGVNY--YQGQGRMKPRHRLMTATALLGRVGLDDMOYFRPHAPADRLDRCFHNADY	85				
QY	545	YGHRA----TEKKMKTRELHR-----ESSNDSITYICPSTFACAOATLGAACRLVEAVLS	595				
	86	VSLFRSTVETPQDDIATLAKRFVNGECCAPFDGLYSCQYVAGG--SVGGAVKTKLNHG--H	141				

OY 596 GEVLNGAAYVRPPGHAEODACGCFEFSNVAVAARHNOTISGHAIRLLIYDMVHNGC 655
 DB 142 DIANNAGGL---HHAKKEASGFCYVNDIVLAI--LELLKXHO-RVLYIDIDHHGDD 194
 OY 656 TOHMFEDDPVLYSLRYDHGTFEPMGDEGASSOIGRAAGTGTVNVAMNGPRMGADY 715
 DB 195 VEEAFPTTDKVMYSFHKF--GDYFP--GTGDDIDVHSGKGYSLNVPDLD-DGIDESTY 249
 OY 716 LAAMHRLVLPDIAEENDELVLVSAGFDAGDPLGGCOVSEGYAHLTHLMGLASGRRI 775
 DB 250 OSLEFKPMGRVMEYFNAGVAVLQCGADSLSGDRIGCNLSIKGAECVRFMRSP-NVPL 308
 OY 776 LILEGGYNLTISSESNAACRSLGDEPPLTLTPRP 812
 DB 309 LLEGGYYTIRNVARCWCYETGVALGHE--LTDKMP 342

RESULT 5

US-09-282-305-2
 ; Sequence 2, Application US/09282305
 ; Patent No. 6287843
 ; GENERAL INFORMATION:
 ; APPLICANT: Baldwin, Donald A.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Crane, Virginia C.
 ; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
 ; FILE REFERENCE: 5718-44,
 ; CURRENT APPLICATION NUMBER: US/09/282,305
 ; PRIOR FILING DATE: 1999-03-31
 ; PRIOR APPLICATION NUMBER: 60/080,563
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 458
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; US-09-282-305-2

Query Match 4.3%; Score 278; DB 4; Length 458;

Best Local Similarity 26.1%; Pred. NO. 1.2e-15; Matches 115; Conservative 73; Mismatches 179; Indels 74; Gaps 21;

OY 500 HEEVPRILRIMCRLEELAGRLTLT-PRPATEALLTCHSAEYVGH- 548
 DB 41 HPMKPRIRIMAHSLVYHGL-HRLLELSRYPASEADIRFHSDDYAFALASATGNPVL 99
 OY 549 --RATEKMKTRLEHRESSNFDIYICPSTFACQALATGAACRLVEAVLSE--VLNGAA 603
 DB 100 DRAIRKRFVNGE--DCPVEFGLF--PFCQASAGSISGAIVKLNK---GDADITVWAG 150
 OY 604 VVRPBGHNAODACGCFEFSNVAVAARHNOTISGHAIRLLIYDMVHNGCQHMEDD 663
 DB 151 GL---HHAKKEASGFCYVNDIVLAI--LELLKXHO-RVLYIDIDHHGDEEAFETT 203
 OY 664 PSVLYSLRHYDHGTFEPMGDEGASSOIGRAAGTGTVNVAMNGPRMGADYLAAMRLV 723
 DB 204 NVMYVSFHKY--GDYFP--GTGDDIDVHSGKGYSLNVPDLD-DGIDESTY 258
 OY 724 LPIAEFNEDELVLVSAGFDAGDPLGGCOVSEGYAHLTHLMGLASGRRIILLEGYN 783
 DB 259 KRYMEYQPDVAVLQCGADSLSGDRIGCNLSIKGAECVRFMRSP-NVPL 317
 OY 784 LNSISMAACRSLGDEPPLTLTPRP 812
 DB 318 IINVAACWCYETAVAAGVPEPMKLPYNDYIYEGPPTLTIQPKSVENLTITDLENIKN 377
 OY 829 RYMRSLRVKVE-----DREGPSSSLVTKKAPQAPKRL---AERMTTREQ 872
 DB 378 MLENI--SKIEHVSTOFHNRPSDEAPBEKEEDMDKRP-PQRSRLMSGAYDSPTEDP 434
 OY 873 KVLGAMGRVTSASFGEESTP 893

DB 435 DSLKS-EGKDVYANFOMKDEP 454

RESULT 6

US-08-528-255A-1
 ; Sequence 1, Application US/08528255A
 ; Patent No. 5659016
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAMURA, YUSUKE
 ; APPLICANT: FUKUKAWA, YOICHI
 ; TITLE OF INVENTION: RPD PROTEIN AND DNA
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLYNN, THELL, BOUTELL & TANIS, P.C.
 ; STREET: 2026 Rambling Road
 ; CITY: Kalamazoo
 ; STATE: Michigan
 ; COUNTRY: USA
 ; ZIP: 49008-1699

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
 COMPUTER: IBM PC/XT/AT Compatible
 OPERATING SYSTEM: MS-DOS 5.0
 SOFTWARE: Wordperfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/528,255A
 FILING DATE: September 14, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP6-227876
 FILING DATE: 22-SEPTEMBER-1994
 APPLICATION NUMBER: JP7-183763
 FILING DATE: 20-JULY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Terryence F. Chapman
 REGISTRATION NUMBER: 32549
 REFERENCE/DOCKET NUMBER: Furuya Case 1335
 TELEPHONE: (616) 381-1156
 TELEFAX: (616) 381-5465
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 482
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 LIBRARY: human fetal lung cDNA library
 US-08-528-255A-1

Query Match 4.3%; Score 277.5; DB 1; Length 482;

Best Local Similarity 23.8%; Pred. NO. 1.5e-15; Matches 110; Conservative 76; Mismatches 210; Indels 67; Gaps 17;

OY 485 YDONMAMHNCIMLMDHHEVPRILRIMCRLEELAGRLTLTTPRPAEALLTCHSAEY 544
 DB 15 YDGGVNGV--YUGGHHKPRIRIMTNTNLLNYGIRKMEIYRPHKAAEEMTKYHSDDY 72
 OY 545 VGHIRATEKMKTRLEHRESSNFDIYICP--STFACQALATGAACRLVEAVLSEGVNG 601
 DB 73 IKFLRSIRPNMSSEYSKQOMRFNVEGDCPVEFGLFEECQSLSTGGS--VASAVKLKNOOTD 130
 OY 602 AAYVRPPG-HHAEODACGCFEFSNVAVAARHNOTISGHAIRLLIYDMVHNGCQHMEDD 660
 DB 131 IAVNWAGGLHNAKKEASGFCYVNDIVLAI--LELLKXHO-RVLYIDIDHHGDEEAF 187
 OY 661 EDDPSVLYSLRHYDHGTFEPMGDEGASSOIGRAAGTGTVNVAMNGPRMGADYLAAMH 720

DB 188 YTTDRMYVSFKY--GEYFP--GTGDLNDIGAGKYYAVNPLR-DGIDDESYEAIK 242

OY 721 RLVLPIAYEPNELVYVSGFDAPRGDPLGGCOVSEGYA-----HILHLGLAS 771

DB 243 PYMSKVMEMFOPSAAVAVLQCGSDSLSGDRGCFNLTKGHAKCVEFKSFLPMLMG--- 299

OY 772 GRILLILEGGYNLTSS-----ESMAACTRSLIGDP-----PLTLPRPLSGAL 817

DB 300 -----GGGYTIRNVARCRITYETAVALDTEIPNELPYNDYEFYFGPDKLHISPSNMTN 352

OY 818 ASITETIQ-VHRRYRSLRVMKVEDREGPSSSKLVTKKAPOPAKPRLA--ERMTTREKKY 874

DB 353 QNTNEYLEKIKORLPENLML-----PHAGVQQAIPEDAIPEESGDEDEDPPDKRI 405

OY 875 LEAGMK-----VTSASFGSEESTPGQTNSETAVALTQD 909

DB 406 SICSSDKRIACEEFSDESEEGGRKNSNPKKARVATEDE 448

RESULT 7

US-08-717-365-1

Sequence 1, Application US/08717365

Patent No. 5763182

GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE

APPLICANT: FURUKAWA, YOICHI

TITLE OF INVENTION: RPD, PROTEIN AND DNA

TITLE OF INVENTION: ENCODING THE SAME

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLYNN, THEL, BOUTELL & TANIS, P.C.

STREET: 2026 Rambling Road

CITY: Kalamazoo

STATE: Michigan

COUNTRY: USA

ZIP: 49008-1699

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage

COMPUTER: IBM PC/XT/AT Compatible

OPERATING SYSTEM: MS-DOS 5.0

SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,365

FILING DATE: 23-SEP-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/528 255

FILING DATE: September 14, 1995

APPLICATION NUMBER: JP6-227876

FILING DATE: 22-SEPTEMBER-1994

APPLICATION NUMBER: JP7-183763

FILING DATE: 20-JULY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teriyence F. Chapman

REGISTRATION NUMBER: 32549

REFERENCE/DOCKET NUMBER: Futuya Case 1335

TELECOMMUNICATION INFORMATION:

TELEPHONE: (616) 381-1156

TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 482

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

LIBRARY: human fetal lung cDNA library

US-08-717-365-1

Query Match 4.3% Score 277.5; DB 1; Length 482;

Best Local Similarity 23.8%; Pred. No. 1.5e-15;

Matches 110; Conservative 76; Mismatches 210; Indels 67; Gaps 17;

OY 485 YQNMNHNCLMDSHHPVORILRIMCRLEELGAGRCUTLPPRPAEALLTCHSAEY 544

DB 15 YDGDVGNV--YYGQGHPRMHRIRMTNHLNLTGLVRKMEIYRPHKNAEMGKHSDDY 72

OY 545 VGHRLATEKMKRRELHRESSNDSIYICP---STPACQALATGACRLVAVSGEVLNG 601

DB 73 IKFLRSIRPDNMSEYSKQHQRFNVGDCPEFDGLFECQLSTGGS--VASAVKLNKQOTD 130

OY 602 AAIVRPPG--HHAEGDAACGCEFNSSVAVAARAHOISGHALRLIYDMVDVHNGNQHM 660

DB 131 IAVNNAAGGHHAKKSASGFCYNDIVLAI--LELIKHYO-RVLYIDIDHGDGVEAF 187

OY 661 EDDPSVLYVSLRHRYDHTFPPMGDEGASSOIGRAAGTGFVNANMGPRGADYLAAMH 720

DB 188 YTTDRMYVSFKY--GEYFP--GTGDLNDIGAGKYYAVNPLR-DGIDDESYEAIK 242

OY 721 RLVLPIAYEPNELVYVSGFDAPRGDPLGGCOVSEGYA-----HILHLGLAS 771

DB 243 PYMSKVMEMFOPSAAVAVLQCGSDSLSGDRGCFNLTKGHAKCVEFKSFLPMLMG--- 299

OY 772 GRILLILEGGYNLTSS-----ESMAACTRSLIGDP-----PLTLPRPLSGAL 817

DB 300 -----GGGYTIRNVARCRITYETAVALDTEIPNELPYNDYEFYFGPDKLHISPSNMTN 352

OY 818 ASITETIQ-VHRRYRSLRVMKVEDREGPSSSKLVTKKAPOPAKPRLA--ERMTTREKKY 874

DB 353 QNTNEYLEKIKORLPENLML-----PHAGVQQAIPEDAIPEESGDEDEDPPDKRI 405

OY 875 LEAGMK-----VTSASFGSEESTPGQTNSETAVALTQD 909

DB 406 SICSSDKRIACEEFSDESEEGGRKNSNPKKARVATEDE 448

RESULT 8

US-09-282-305-10

Sequence 10, Application US/09282305

Patent No. 6287843

GENERAL INFORMATION:

APPLICANT: Baldwin, Donald A.

APPLICANT: Briggs, Steven P.

TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses

FILE REFERENCE: 5718-44,

CURRENT APPLICATION NUMBER: US/09/282,305

PRIOR FILING DATE: 1999-03-31

PRIOR APPLICATION NUMBER: 60/080,563

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 10

LENGTH: 432

TYPE: PRT

ORGANISM: Zea mays

US-09-282-305-10

Query Match 3.8% Score 242; DB 4; Length 432;

Best Local Similarity 25.9%; Pred. No. 1.5e-12;

Matches 87; Conservative 51; Mismatches 158; Indels 40; Gaps 13;

OY 469 LPILTWPIVLSRTGLVYDQNMNHNCLMDSHHPVORILRIMCRLEELGAGRCUTLPP 528

DB 5 LPITVITPIVGVGVNV-----FGPNHPRMHRICMTHHLVLSGLQKMEIYR 54

OY 529 RPAEAEALLTCHSAEYVGLRA---TEKMKTRRELHRESSNDSIYICP---STPACQAL 581

DB 55 HKAVPIELAOPHSADYVEFLHRTIPDSOHLVASELTRYMLGSD---CPVPNLFFPQDI 110

OY 582 ATGA---ACRLVEAVLSEVNLGAAVVRPPGHAAODAACGCFNSVAVAAHQAOTISG 638

DB 111 YAGTIDAAARRINRHKICDAINMAGL---HHAKECASGFCYINDIVLGI--LELLKY 164

Db 541 VTTPTNATSPITLGIKTSPTSAVTTPTNATSPITLKIPTSATVT-----PPNAT-SPT 594

QY 920 LAQISEAIGAMLGOTT-----SEAVGATPDQTSSEVVGAI---LDQTSSEDAV 971

Db 595 LKRTSPISAV-----TTPPNATGPTVGETSPDANATNHTLGGSPPTPVTSOPKNAT 647

QY 972 GGATLGQ-----TTSEAVGATLAQITISEAMEGAT--LDQTSSEAVGGTELIQ--TP 1022

Db 648 SAVTGGHNTSSSSMSLRSSNPETLSPSTONSHTMPLTSAHPTGGENITQVTP 707

QY 1023 LASTSDH-QTPPTSVOGTTPOI-----SPSTLIGSLTLELGSOGASQASQAP-GE 1074

Db 708 ASISTHVTSSPEPRPGTTSQASGPGNSSTKPGEVNVTK-GTPPNATSPQAPSQK 766

QY 1075 NLT-----GEA-----AGGDMADSMMLQSGSLDQAFY---AVTPLP 1111

Db 767 TAVPTVSTGKANSTTGKHTTG---HGARTSTPTDYGDDSTTPRP 812

RESULT 11

US-09-328-599A-1

Sequence 1, Application US/09328599A

Patent No. 6432679

GENERAL INFORMATION:

APPLICANT: MOND, James J. and Lees, Andrew

TITLE OF INVENTION: Enhancement of B Cell Activation by

TITLE OF INVENTION: Co-Ligation of Receptors for Antigen and Complement C3d

TITLE OF INVENTION: Using EBV gp350/220 or EBV gp350/220 Peptide Adjuvants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner, L.L.P.

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/328,599A

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Fordis, Jean B.

REGISTRATION NUMBER: 32,984

REFERENCE/DOCKET NUMBER: 04995.6025-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 907 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-328-599A-1

Query Match 2.4%; Score 155.5; DB 4; Length 907;

Best Local Similarity 21.0%; Pred. No. 0.00021;

Matches 162; Conservative 87; Mismatches 292; Indels 229; Gaps 43;

QY 484 VYDQNMNHCNLMDSHHPVORILRLMCRLEELGIAGRCFLTPRATSEALLTGSAAE 543

Db 130 VYQDVVG--TAM-CHAEKQNPY-----LIPETVPIYKWNQCNSTN 169

QY 544 YVGHLEATEKRTREILHRESSNDSIYICSTF-----ACAQLATG----- 584

Db 170 ITAVYVRAQGLDVTLLPSTLPSADSNSFVTEMLGNEDIECIMEDGEISIVLPQDKFN 229

QY 585 AACRLVEA-VLSEGVINGAAYVRPBGHAEQDAACFCFPNSVAVAAHQAOTISGAARI 643

Db 230 ITCSGESHPGSGILTSTSPVATP-----IPGTAYV--SLRLPRPVSRELGN--SI 280

QY 644 LLYDMDVHHGNG-----TQMFEDDPSVLYSLHARDHCTF-E 680

Db 281 LTV-----FYSGNPKKASGGYCIQSNIVSEDELPASQDMPTNTDITYVG---DNATVSY 333

QY 681 PM-GDEGASSQIGRAAGTFTVNVAMGPRMDADADYLAAMHRLVPLIAVEFNEDELVLSA 739

Db 334 PAVTSEDAANS-----PVTYTAFWAMPNNETDEKCM-----TLTS- 370

QY 740 GFDAARGDPLGCGOVSPEYA-----HLTHLMGLASGRILLILEGYNLTS-----IS 788

Db 371 -----GTP-SCCENISGAFAASNRTFDIVSGIGTAP-KTLITTRATNATVTHKVIYS 422

QY 789 BSMACSTSL-----LGDP-----PPLTLTP-----RPLSGALA 818

Db 423 KAPESTTSPITLNTGFPADPNTTGLPSTHVPNTLTAASGTGPTVSTADVTSPTPAGTT 482

QY 819 SITETIOVHRRYRSLRWKVEDREGSSSKLVTKKAPQAPARPLA-----ER 866

Db 483 SCASPVTPSPSPWDNGTESKAPDM--TSTSPVTTPTPNATSPTPAVTTPTPNATSPTPA 540

QY 867 MTRKKVLEAGMGKVTASGFESESTP-----GQTSNVAVALTQDQSEAAATGAT 919

Db 541 VTTPTNATSPITLGIKTSPTSAVTTPTNATSPITLKIPTSATVT-----PPNAT-SPT 594

QY 920 LAQISEAIGAMLGOTT-----SEAVGATPDQTSSEVVGAI---LDQTSSEDAV 971

Db 595 LKRTSPISAV-----TTPPNATGPTVGETSPDANATNHTLGGSPPTPVTSOPKNAT 647

QY 972 GGATLGQ-----TTSEAVGATLAQITISEAMEGAT--LDQTSSEAVGGTELIQ--TP 1022

Db 648 SAVTGGHNTSSSSMSLRSSNPETLSPSTONSHTMPLTSAHPTGGENITQVTP 707

QY 1023 LASTSDH-QTPPTSVOGTTPOI-----SPSTLIGSLTLELGSOGASQASQAP-GE 1074

Db 708 ASISTHVTSSPEPRPGTTSQASGPGNSSTKPGEVNVTK-GTPPNATSPQAPSQK 766

QY 1075 NLT-----GEA-----AGGDMADSMMLQSGSLDQAFY---AVTPLP 1111

Db 767 TAVPTVSTGKANSTTGKHTTG---HGARTSTPTDYGDDSTTPRP 812

RESULT 12

PCT-US95-04611A-19

Sequence 19, Application PC/TUS9504611A

GENERAL INFORMATION:

APPLICANT: Spaete, Richard and Jackman, Winthrop, T.

TITLE OF INVENTION: Non Splicing Variants of gp350/220

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04611A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/229,291

FILING DATE: April 18, 1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Luann Cseer
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: AVIR-003/0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5163
 TELEFAX: 415-857-0663
 TELEX: 380816 COOLEYPA
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 907 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-04611A-19

Query Match 2.4%; Score 155.5; DB 5; Length 907;
 Best Local Similarity 21.0%; Pred. No. 0.00021;
 Matches 162; Conservative 87; Mismatches 292; Indels 229; Gaps 43;

484 VTDOMNANHCLMDSHHEVPORILRIMCRLEELGLAGRCILTPRPATEALLTCHSAE 543
 130 VYFQDVFQ--TMM-CHHAEMQNPVY-----LIPETVPIKMDNCNSTN 169
 544 YVGHRLATEKMKTRRELHRESSNDSITYICPSTF-----ACAQLATG----- 584
 170 ITAVVRAOGLDVTLPRLPTSAODSNFVKTMLGNEIDIECIMDEGEISQVLPGDNKF 229
 585 AACRLVEA-VLSGEVINGAAVVRPGHHAEDDAACGCFPNVAVAAHQAOTISGHARI 643
 230 ITCGESHVPSGGILITSTSPVATP-----IPGTGAY--SLRLPRVPSRLGN--SI 280
 644 LIVDMVHHNG-----TOHMFEDDPSVLYSLHRYDHGT-F 680
 281 LYV---FYSGNGPKASGSDYCIQSNIVFSDIPLASQDMPTNTDITYG---DNATYSV 333
 681 PM-GDEGASSOIGRAAGTGFYVAVANGPRMGDADYLAAMHRLVLAIEFNPDELVLSA 739
 334 PAVTSEDANS-----PNVTYAFWAMPNNTETDFCKW-----TLTS- 370
 740 GFDAARGLDGLGCOVSPREGYA-----HLTHLMGLASGRILLLEGYNLTS-----IS 788
 371 -----GTF--SGCENISGAFASNRFTDIYSGIGLTP--KTLITRTATNATTTTHKVIYS 422
 789 ESMACRSL-----LQDP-----PPLTLTP-----RPLSGALA 818
 423 KAPESTTSPPLNTGTFADPNTTGLPSTHVPNTLTAASSTPTVSTADVTSPTPAGTT 482
 819 STETIOVHRKRWLSLRKMKVEDREGPSSSKLVTKKAPAKPRLA-----ER 866
 483 SGASPVTPSPSPMDNTESEKAPDM--TSTSTPTPTTPNATSPRAVATTPPNATSPRA 540
 867 MTPREKVLKMGKVTASASGEESTP-----GQTSERAVVALTDQDSEATGAT 919
 541 VTTPTPNATSPPLTKISTPTSAVTTPTPNATSPPLTKISTPTSAVTT-----PPLNAT--SPT 594
 920 LAQITSEAAIGAMAGOTT-----SEAVGATPDQTTSEETVGAI---LDQTSSEAV 971
 595 LKGTSPISAV-----TTPPNATGPTVGETSPOANATNTLGGTSTPTVYTSTPQKAT 647
 972 GGATLGO-----TTSSEAVGATLAQITSEAMEGAT--LDQTSSEAPGTELIQ--TP 1022
 648 SAVTTGQHNTTSSSTSSMLSPSSNPETLSPSTSDNSTSHMPLLSAHTGENTITQVTP 707
 1023 LASTTDH-QTPPTSPVQCTPQI-----SPSTLIGSLRIEELSGSAGASECAP--GEE 1074
 708 ASISTHVTSSSPRPGTTSQASGPGNSSSTKRGEEVNTK--GTPPNATSPQAPSGOK 766
 1075 NL-----GEA---AGQDMADSMMLQSGRLDQAIFF---AVPPLP 1111
 767 TAVPTVSTGKASTTGKHTTG-----HGKRTSTETPTDYGGSSTTPRP 812

RESULT 13

US-09-556-706B-2

Sequence 2, Application US/09556706B

Patent No. 6458364

GENERAL INFORMATION:

APPLICANT: Spaete, Richard

APPLICANT: Jackman, Winthrop

TITLE OF INVENTION: NON SPLICING VARIANTS OF GP350/220

FILE REFERENCE: 7682-050-999

CURRENT APPLICATION NUMBER: US/09/556,706B

CURRENT FILING DATE: 2000-04-24

PRIOR APPLICATION NUMBER: 08/783,774

PRIOR FILING DATE: 1997-01-15

PRIOR APPLICATION NUMBER: 08/229,291

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 878

TYPE: PRT

ORGANISM: Virus

FEATURE:

OTHER INFORMATION: gp350

US-09-556-706B-2

Query Match 2.4%; Score 150.5; DB 4; Length 878;
 Best Local Similarity 21.7%; Pred. No. 0.00053;
 Matches 163; Conservative 79; Mismatches 297; Indels 213; Gaps 42;

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 130 VYFQDVFQ--TMM-CHHAEMQNPVY-----LIPETVPIKMDNCNSTN 169
 544 YVGHRLATEKMKTRRELHRESSNDSITYICPSTF-----ACAQLATG----- 584
 170 ITAVVRAOGLDVTLPRLPTSAODSNFVKTMLGNEIDIECIMDEGEISQVLPGDNKF 229
 585 AACRLVEA-VLSGEVINGAAVVRPGHHAEDDAACGCFPNVAVAAHQAOTISGHARI 643
 230 ITCGESHVPSGGILITSTSPVATP-----IPGTGAY--SLRLPRVPSRLGN--SI 280
 644 LIVDMVHHNG-----TOHMFEDDPSVLYSLHRYDHGT-F 680
 281 LYV---FYSGNGPKASGSDYCIQSNIVFSDIPLASQDMPTNTDITYG---DNATYSV 333
 681 PM-GDEGASSOIGRAAGTGFYVAVANGPRMGDADYLAAMHRLVLAIEFNPDELVLSA 739
 334 PAVTSEDANS-----PNVTYAFWAMPNNTETDFCKW-----TLTS- 370
 740 GFDAARGLDGLGCOVSPREGYA-----HLTHLMGLASGRILLLEGYNLTS-----IS 788
 371 -----GTF--SGCENISGAFASNRFTDIYSGIGLTP--KTLITRTATNATTTTHKVIYS 422
 789 ESMACRSL-----LQDP-----PPLTLTP-----RPLSGALA 818
 423 KAPESTTSPPLNTGTFADPNTTGLPSTHVPNTLTAASSTPTVSTADVTSPTPAGTT 482
 819 STETIOVHRKRWLSLRKMKVEDREGPSSSKLVTKKAPAKPRLAEMRTTRKKVLEAG 878
 483 SGASPVTPSPSPMDNTESEKAPDM--TSTSTPTPTTPNATSPRAVATTPPNATSPRA 540
 879 MGVTSASASGEESTPGQTSERAVVALTDQDSEATGATLAQITSEAAI-----GG 931
 539 PAVTTPTPNATSPPLTKISTPTSAVTT-----PPLNAT--SPTLTKISTPTSAVTTPTPNAT 592
 932 AMAGQTSSEAVGATPDQTTSEETVGAIILDQTSSEAVGATLIGQTTSEAV-----GG 987
 593 PTLGKTSPTSAVTTPTPNAT-----GPTVGETSPOANATNTLGGTSTPTVYTSTPQKAT 645
 968 ATLQITSE---AAMEGATLIDQTSSEAP---GTEFLIO--TPLASTDH-QTPPTSPVQ 1039
 646 ATSAVTTGQHNPSSNPETLSPSTSDNSTSHMGENITQVTPASISTHVTSSSPRPG 705

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 14:49:28 ; Search time 56 Seconds
(without alignments)
2239.945 Million cell updates/sec

Title: US-09-800-187-6
Perfect score: 6397
Sequence: 1 MTSTGQDSTTRRORRORNP.....LDVKNIAHQNFGEEDMPHPH 1215

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 392085 segs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6397	100.0	1215	US-09-976-280A-4	Sequence 4, Appl1
2	6397	100.0	1215	US-09-976-280A-22	Sequence 22, Appl1
3	6375	99.7	1215	US-09-817-913-11	Sequence 11, Appl1
4	6375	99.7	1215	US-09-817-538-11	Sequence 11, Appl1
5	1125	17.6	673	US-09-976-280A-2	Sequence 2, Appl1
6	809	12.6	687	US-09-976-280A-3	Sequence 3, Appl1
7	805.5	12.6	967	US-09-563-728A-30	Sequence 30, Appl1
8	805.5	12.6	1084	US-10-072-094-7	Sequence 7, Appl1
9	805.5	12.6	1084	US-10-173-539-12	Sequence 12, Appl1
10	801.5	12.5	967	US-09-817-913-7	Sequence 7, Appl1
11	801.5	12.5	967	US-09-817-913-7	Sequence 7, Appl1
12	788	12.3	706	US-10-072-094-6	Sequence 6, Appl1
13	778.5	12.2	716	US-09-563-728A-32	Sequence 32, Appl1
14	778.5	12.2	1122	US-10-072-094-8	Sequence 8, Appl1
15	778.5	12.2	1122	US-10-072-094-91	Sequence 91, Appl1
16	767.5	12.0	717	US-09-817-913-9	Sequence 9, Appl1
17	767.5	12.0	717	US-09-817-538-9	Sequence 9, Appl1
18	763	11.9	780	US-10-072-094-93	Sequence 93, Appl1
19	763	11.9	1069	US-10-072-094-87	Sequence 87, Appl1

20	755.5	11.8	855	10	US-09-817-913-13	Sequence 13, Appl1
21	755.5	11.8	855	10	US-09-817-538-13	Sequence 13, Appl1
22	750.5	11.7	855	9	US-10-072-094-9	Sequence 9, Appl1
23	722	11.3	967	9	US-10-173-539-6	Sequence 6, Appl1
24	722	11.3	1011	9	US-10-072-094-89	Sequence 89, Appl1
25	722	11.3	1011	9	US-10-173-539-2	Sequence 2, Appl1
26	619.5	9.7	1141	9	US-10-072-094-107	Sequence 107, Appl1
27	561.5	8.8	342	9	US-09-911-150-4	Sequence 4, Appl1
28	419	6.5	835	9	US-10-173-539-8	Sequence 8, Appl1
29	419	6.5	879	9	US-10-072-094-90	Sequence 90, Appl1
30	419	6.5	879	9	US-10-173-539-4	Sequence 4, Appl1
31	418.5	6.5	163	9	US-10-072-094-4	Sequence 4, Appl1
32	390	6.1	335	10	US-09-971-309-80	Sequence 80, Appl1
33	292	4.6	517	10	US-09-883-720-8	Sequence 8, Appl1
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35	291	4.5	377	10	US-09-817-913-15	Sequence 15, Appl1
36	291	4.5	377	10	US-09-817-538-15	Sequence 15, Appl1
37	290.5	4.5	344	10	US-09-883-720-6	Sequence 6, Appl1
38	286.5	4.5	344	10	US-09-815-242-5059	Sequence 5059, Appl1
39	286	4.5	150	9	US-09-911-150-6	Sequence 6, Appl1
40	278	4.3	458	10	US-09-883-720-2	Sequence 2, Appl1
41	277.5	4.3	482	9	US-09-563-728A-24	Sequence 24, Appl1
42	277.5	4.3	488	10	US-09-925-300-1563	Sequence 1563, Appl1
43	277	4.3	481	10	US-09-817-913-1	Sequence 1, Appl1
44	277	4.3	481	10	US-09-817-538-1	Sequence 1, Appl1
45	277	4.3	576	10	US-09-347-331-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1	US-09-976-280A-4	Sequence 4, Application US/0976280A
1	Sequence 4, Application US/0976280A	Patent No. US20020115177A1
2	Patent No. US20020115177A1	GENERAL INFORMATION:
3	GENERAL INFORMATION:	Applicant: Zhu, Zhimin
4	Applicant: Zhu, Zhimin	TITLE OF INVENTION: Regulation of Human Histone Deacetylase
5	TITLE OF INVENTION: Regulation of Human Histone Deacetylase	FILE REFERENCE: 004974.00590
6	FILE REFERENCE: 004974.00590	CURRENT APPLICATION NUMBER: US/09/976, 280A
7	CURRENT APPLICATION NUMBER: US/09/976, 280A	CURRENT FILING DATE: 2001-10-15
8	CURRENT FILING DATE: 2001-10-15	PRIOR APPLICATION NUMBER: US 60/239, 928
9	PRIOR APPLICATION NUMBER: US 60/239, 928	PRIOR FILING DATE: 2000-10-13
10	PRIOR FILING DATE: 2000-10-13	NUMBER OF SEQ ID NOS: 25
11	NUMBER OF SEQ ID NOS: 25	SOFTWARE: FastSeq for Windows Version 4.0
12	SOFTWARE: FastSeq for Windows Version 4.0	SEQ ID NO 4
13	SEQ ID NO 4	LENGTH: 1215
14	LENGTH: 1215	TYPE: PRT
15	TYPE: PRT	ORGANISM: Homo sapiens
16	ORGANISM: Homo sapiens	US-09-976-280A-4
17	US-09-976-280A-4	Query Match
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19	Best Local Similarity 100.0%; Score 6397; DB 10; Length 1215;	Matches 1215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20	Matches 1215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
21		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
22		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
23		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
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35		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
36		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
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40		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
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47		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
48		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
49		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
50		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
51		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
52		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
53		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
54		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
55		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
56		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
57		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
58		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
59		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
60		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
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62		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
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64		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
65		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
66		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
67		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
68		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
69		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
70		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
71		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
72		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
73		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
74		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
75		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
76		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
77		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
78		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
79		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
80		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
81		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
82		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
83		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
84		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
85		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
86		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
87		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
88		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
89		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
90		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
91		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
92		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
93		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
94		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
95		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
96		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
97		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
98		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
99		QY 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60
100		DB 1 MTSTGQDSTTRRORRORNPSPDPDSVTSKRNIKKGAVPSPINLAEVKKKKKKK 60

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Db      241 KHRIRVLYDMVHNGOGTQTFEDDPSVLYFSIHRYEGRFPHHKASNMSTGFGOG 300
Qy      301 OGTTINPNNQVGMGRADYIAAFLVLLPVALFEFOPOLVYAAGFDALOGDPKEMATP 360
Db      301 OGTTINPNNQVGMGRADYIAAFLVLLPVALFEFOPOLVYAAGFDALOGDPKEMATP 360
Qy      361 AGFAOLTHLMGLAGKLLISLEGYMLRALAEVSASLHTLLGDPGMLESPPACRSA 420
Db      361 AGFAOLTHLMGLAGKLLISLEGYMLRALAEVSASLHTLLGDPGMLESPPACRSA 420
Qy      421 QASVSCALELFEFWEVLVSTETVERDNNEEDNVESEEGPWEPPVLLTPVYQSR 480
Db      421 QASVSCALELFEFWEVLVSTETVERDNNEEDNVESEEGPWEPPVLLTPVYQSR 480
Qy      481 TGLVYDQNMNHNCLMDSHHPREVPORILRLIMCRLEELGLAGRCITLTPRPAATEMLTCH 540
Db      481 TGLVYDQNMNHNCLMDSHHPREVPORILRLIMCRLEELGLAGRCITLTPRPAATEMLTCH 540
Qy      541 SAETVGHRLATEKMKTRRELHRESSNFDISYICPSTFACQALATGACRLVEAVLSGEVLN 600
Db      541 SAETVGHRLATEKMKTRRELHRESSNFDISYICPSTFACQALATGACRLVEAVLSGEVLN 600
Qy      601 GAAVVRPBGHHAQDAAACGCFPNVAVAARHAQOTISGHLRLILYDMVHNGTGHMF 660
Db      601 GAAVVRPBGHHAQDAAACGCFPNVAVAARHAQOTISGHLRLILYDMVHNGTGHMF 660
Qy      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Db      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Qy      721 RLVLPIAYEFNPBELVLYSAGFDARBDPLGCGVSPBGVAHLTHLMGLASGRILLLEG 780
Db      721 RLVLPIAYEFNPBELVLYSAGFDARBDPLGCGVSPBGVAHLTHLMGLASGRILLLEG 780
Qy      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASITETIOVHRRYWSLRVMKVE 840
Db      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASITETIOVHRRYWSLRVMKVE 840
Qy      841 DREGSSSKLYTKKAPQAPAKPRLAERMTTREKKVLAAGMGKVSASFGSESTGGOTNSET 900
Db      841 DREGSSSKLYTKKAPQAPAKPRLAERMTTREKKVLAAGMGKVSASFGSESTGGOTNSET 900
Qy      901 AVVALTODOPSEAAATGATLAOTISPAIIGAMIGOTTSEAVGATLPDQTTSEETVGA 960
Db      901 AVVALTODOPSEAAATGATLAOTISPAIIGAMIGOTTSEAVGATLPDQTTSEETVGA 960
Qy      961 IILDOTTSEAVGATLGOTTSEAVGATLAOTISPAAMEGATLIDOTTSEABGTGLIO 1020
Db      961 IILDOTTSEAVGATLGOTTSEAVGATLAOTISPAAMEGATLIDOTTSEABGTGLIO 1020
Qy      1021 TPLASTDHPQPTSPVOGTTPOISPTLIGSLRTLELGSSEOGASESQAPEENILGSA 1080
Db      1021 TPLASTDHPQPTSPVOGTTPOISPTLIGSLRTLELGSSEOGASESQAPEENILGSA 1080
Qy      1081 AGGODMADSMLMQSGRGLTDOAIFYAVPLPWCPRHLVAVCPPIPAIGLIDVTOPOCGDCGCTIO 1140
Db      1081 AGGODMADSMLMQSGRGLTDOAIFYAVPLPWCPRHLVAVCPPIPAIGLIDVTOPOCGDCGCTIO 1140
Qy      1141 ENMVCLSCYQYCGRTINGHMLQHHGNSGHPVLSTIDLSANCYCCQAVVHHQALLDVKN 1200
Db      1141 ENMVCLSCYQYCGRTINGHMLQHHGNSGHPVLSTIDLSANCYCCQAVVHHQALLDVKN 1200
Qy      1201 IAHONKFGEDMHPH 1215
Db      1201 IAHONKFGEDMHPH 1215

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RESULT 2
US-09-976-280A-22

; Sequence 22, Application US/09976280A

; Patent No. US20020115177A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Zhimin

1

```

; TITLE OF INVENTION: Regulation of Human Histone Deacetylase
; FILE REFERENCE: 004974.00590
; CURRENT APPLICATION NUMBER: US/09/976.280A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,928
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1215
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-976-280A-22

Query Match      100.0%; Score 6397; DB 10; Length 1215;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MTSFGDSTTRORRSRONPQSPDSSVTSKRNIKKGAVPRSTPNLAEVYKKKKKGLG 60
Db      1 MTSFGDSTTRORRSRONPQSPDSSVTSKRNIKKGAVPRSTPNLAEVYKKKKKGLG 60
Qy      61 QAMEEDLIVGLQMDLMEALAGTGLVDEQLEFHCILMDDSPPEGPERLHAATKEOLI 120
Db      61 QAMEEDLIVGLQMDLMEALAGTGLVDEQLEFHCILMDDSPPEGPERLHAATKEOLI 120
Qy      121 QEGLLDRCVSFOARFAKEELIMVHSEYIDIMETTOYMBGELRVADYDYSYLHNS 180
Db      121 QEGLLDRCVSFOARFAKEELIMVHSEYIDIMETTOYMBGELRVADYDYSYLHNS 180
Qy      181 YSCCLASGSVLRIVDAVLAETIRNGAAIIRPCHHQAQSLMDGTCMFNVAARVAARV 240
Db      181 YSCCLASGSVLRIVDAVLAETIRNGAAIIRPCHHQAQSLMDGTCMFNVAARVAARV 240
Qy      241 KHRIRVLYDMVHNGOGTQTFEDDPSVLYFSIHRYEGRFPHHKASNMSTGFGOG 300
Db      241 KHRIRVLYDMVHNGOGTQTFEDDPSVLYFSIHRYEGRFPHHKASNMSTGFGOG 300
Qy      301 OGTTINPNNQVGMGRADYIAAFLVLLPVALFEFOPOLVYAAGFDALOGDPKEMATP 360
Db      301 OGTTINPNNQVGMGRADYIAAFLVLLPVALFEFOPOLVYAAGFDALOGDPKEMATP 360
Qy      361 AGFAOLTHLMGLAGKLLISLEGYMLRALAEVSASLHTLLGDPGMLESPPACRSA 420
Db      361 AGFAOLTHLMGLAGKLLISLEGYMLRALAEVSASLHTLLGDPGMLESPPACRSA 420
Qy      421 QASVSCALELFEFWEVLVSTETVERDNNEEDNVESEEGPWEPPVLLTPVYQSR 480
Db      421 QASVSCALELFEFWEVLVSTETVERDNNEEDNVESEEGPWEPPVLLTPVYQSR 480
Qy      481 TGLVYDQNMNHNCLMDSHHPREVPORILRLIMCRLEELGLAGRCITLTPRPAATEMLTCH 540
Db      481 TGLVYDQNMNHNCLMDSHHPREVPORILRLIMCRLEELGLAGRCITLTPRPAATEMLTCH 540
Qy      541 SAETVGHRLATEKMKTRRELHRESSNFDISYICPSTFACQALATGACRLVEAVLSGEVLN 600
Db      541 SAETVGHRLATEKMKTRRELHRESSNFDISYICPSTFACQALATGACRLVEAVLSGEVLN 600
Qy      601 GAAVVRPBGHHAQDAAACGCFPNVAVAARHAQOTISGHLRLILYDMVHNGTGHMF 660
Db      601 GAAVVRPBGHHAQDAAACGCFPNVAVAARHAQOTISGHLRLILYDMVHNGTGHMF 660
Qy      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Db      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Qy      721 RLVLPIAYEFNPBELVLYSAGFDARBDPLGCGVSPBGVAHLTHLMGLASGRILLLEG 780
Db      721 RLVLPIAYEFNPBELVLYSAGFDARBDPLGCGVSPBGVAHLTHLMGLASGRILLLEG 780
Qy      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASITETIOVHRRYWSLRVMKVE 840
Db      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASITETIOVHRRYWSLRVMKVE 840

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QY 841 DREGSSSKLVTKKAPAPKAPRLAERMTRREKKVLEAGMGKVTASFGSESTPGQTNSET 900
DB 841 DREGSSSKLVTKKAPAPKAPRLAERMTRREKKVLEAGMGKVTASFGSESTPGQTNSET 900
QY 901 AVVALTOPDOPSEAAATGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
DB 901 AVVALTOPDOPSEAAATGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
QY 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
DB 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
QY 1021 TPLASSTHQPPTSPVQGTTPQISPTLSIGLRTLEGSSEOGASESQAPGEENLIGEA 1080
DB 1021 TPLASSTHQPPTSPVQGTTPQISPTLSIGLRTLEGSSEOGASESQAPGEENLIGEA 1080
QY 1081 AGGODMADSMLOGSRGLTDOAIFYATPLPMPCHLVAVCPPIPAAGLDVTPCGDCGTIO 1140
DB 1081 AGGODMADSMLOGSRGLTDOAIFYATPLPMPCHLVAVCPPIPAAGLDVTPCGDCGTIO 1140
QY 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
DB 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
QY 1201 IAHONKFGEDMPHPH 1215
DB 1201 IAHONKFGEDMPHPH 1215

RESULT 3
US-09-817-913-11
; Sequence 11, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besteman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1215
; TYPE: PRT
; ORGANISM: Human
US-09-817-913-11

Query Match 99.7%; Score 6375; DB 10; Length 1215;
Best local Similarity 99.3%; Pred. No. 0;
Matches 1206; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTGODSTTRRQRSRONFPOSPDSSVTSKRNIRKGAVPRSIPNLAEVKKKMKKLG 60
DB 1 MSTGODSTTRRQRSRONFPOSPDSSVTSKRNIRKGAVPRSIPNLAEVKKKMKKLG 60
QY 61 QAMEEELIYGLQMDLLEBALAGTGLVDEOLNEFHCLMDDSFPEGPERRHAIRKQLI 120
DB 61 QAMEEELIYGLQMDLLEBALAGTGLVDEOLNEFHCLMDDSFPEGPERRHAIRKQLI 120
QY 121 QEBGLDRCVFOARPAKEKELMLVHSLLEYIDIMETQYMNNEGELRYLADYDYSYLHPNS 180
DB 121 QEBGLDRCVFOARPAKEKELMLVHSLLEYIDIMETQYMNNEGELRYLADYDYSYLHPNS 180
QY 181 YSCACLASGSVTLVAVLGAETIRNGMAITRPGHHAQHSIMDGYCMFNHVAVARYAOQ 240
DB 181 YSCACLASGSVTLVAVLGAETIRNGMAITRPGHHAQHSIMDGYCMFNHVAVARYAOQ 240
QY 241 KHRIRRVLLVDMVDVHHGQGTQTFDODPSVLYFSIHRYEQGRFWPHLKASNWSITGFGOG 300

DB 241 KHRIRRVLLVDMVDVHHGQGTQTFDODPSVLYFSIHRYEQGRFWPHLKASNWSITGFGOG 300
QY 301 QGYTINVPNNQGMADADYIAAFILHVLVLEFOPOLVLYVAAGFALOGDPGEMAAATP 360
DB 301 QGYTINVPNNQGMADADYIAAFILHVLVLEFOPOLVLYVAAGFALOGDPGEMAAATP 360
QY 361 AGFAOLTHILMGLAGKLLISLEGYNLRALAEVGSASLHTLLGDPCPMLESFAPCRSA 420
DB 361 AGFAOLTHILMGLAGKLLISLEGYNLRALAEVGSASLHTLLGDPCPMLESFAPCRSA 420
QY 421 QASVSCALALEPPEVLYVRSYETVBRDMEDNVSESEEGPWEPPVLPILTWPYQSR 480
DB 421 QASVSCALALEPPEVLYVRSYETVBRDMEDNVSESEEGPWEPPVLPILTWPYQSR 480
QY 481 TGLVYDQNMANNCLNMDSHHPVORILRIMCRLEBLGAGRCILTLTPPATBAELLTCH 540
DB 481 TGLVYDQNMANNCLNMDSHHPVORILRIMCRLEBLGAGRCILTLTPPATBAELLTCH 540
QY 541 SAEYVGHILRAVEKMKTRRELIHRESSNFDIYICPSTFACAOLATGAACRLVEAVLSEVLN 600
DB 541 SAEYVGHILRAVEKMKTRRELIHRESSNFDIYICPSTFACAOLATGAACRLVEAVLSEVLN 600
QY 601 GAAVVRPPGHNAEDQACGFCFFNSVAVARAQOTISGHALRILLYDMVDVHHGNGTOHMF 660
DB 601 GAAVVRPPGHNAEDQACGFCFFNSVAVARAQOTISGHALRILLYDMVDVHHGNGTOHMF 660
QY 661 EDDPSVLVYSLHRYHGFEPFPGDGSASQIGRAAGTGTVVAVNMPGADYLAANH 720
DB 661 EDDPSVLVYSLHRYHGFEPFPGDGSASQIGRAAGTGTVVAVNMPGADYLAANH 720
QY 721 RLVLPIAIEFNEBELVLSAGFEDARGDPLGCGOVSPGYAHLTHILMGLASGRILILLEG 780
DB 721 RLVLPIAIEFNEBELVLSAGFEDARGDPLGCGOVSPGYAHLTHILMGLASGRILILLEG 780
QY 781 GYNLTSISESMAACTRSILGDPPLTLPRPLSGALASITETTIOVHRRYWSLRVAKYE 840
DB 781 GYNLTSISESMAACTRSILGDPPLTLPRPLSGALASITETTIOVHRRYWSLRVAKYE 840
QY 841 DREGSSSKLVTKKAPAPKAPRLAERMTRREKKVLEAGMGKVTASFGSESTPGQTNSET 900
DB 841 DREGSSSKLVTKKAPAPKAPRLAERMTRREKKVLEAGMGKVTASFGSESTPGQTNSET 900
QY 901 AVVALTOPDOPSEAAATGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
DB 901 AVVALTOPDOPSEAAATGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
QY 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
DB 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
QY 1021 TPLASSTHQPPTSPVQGTTPQISPTLSIGLRTLEGSSEOGASESQAPGEENLIGEA 1080
DB 1021 TPLASSTHQPPTSPVQGTTPQISPTLSIGLRTLEGSSEOGASESQAPGEENLIGEA 1080
QY 1081 AGGODMADSMLOGSRGLTDOAIFYATPLPMPCHLVAVCPPIPAAGLDVTPCGDCGTIO 1140
DB 1081 AGGODMADSMLOGSRGLTDOAIFYATPLPMPCHLVAVCPPIPAAGLDVTPCGDCGTIO 1140
QY 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
DB 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
QY 1201 IAHONKFGEDMPHPH 1215
DB 1201 IAHONKFGEDMPHPH 1215

RESULT 4
US-09-817-538-11
; Sequence 11, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:

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; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1215
; TYPE: prt
; ORGANISM: Human
; US-09-817-538-11

Query Match      99.7%; Score 6375; DB 10; Length 1215;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1206; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

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DB      1 MTSTGQDSTTRQRSSRONPOSPPODSSVTSKRNIKGAVPSPISPLAEVKKKKKKKXKLG 60
QY      61 QAMEEDLVGLQGMNLAEALAGTGLVLDSEQLNEFHCLMDSPFEGEERLHAKEQL 120
DB      61 QAMEEDLVGLQGMNLAEALAGTGLVLDSEQLNEFHCLMDSPFEGEERLHAKEQL 120
QY      121 QEGILDRCVSPQAREAEKEELMLVHSLEYIDLMETTYOANNEGELRYLAATYDSVYLHPS 180
DB      121 QEGILDRCVSPQAREAEKEELMLVHSLEYIDLMETTYOANNEGELRYLAATYDSVYLHPS 180
QY      121 QEGILDRCVSPQAREAEKEELMLVHSLEYIDLMETTYOANNEGELRYLAATYDSVYLHPS 180
DB      121 QEGILDRCVSPQAREAEKEELMLVHSLEYIDLMETTYOANNEGELRYLAATYDSVYLHPS 180
QY      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
DB      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
QY      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
DB      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
QY      241 KHRIRRVLIYMDVYHGGTQFTPODPSVLFSTRHOGKRFWPLKASNMSTTFGGG 300
DB      241 KHRIRRVLIYMDVYHGGTQFTPODPSVLFSTRHOGKRFWPLKASNMSTTFGGG 300
QY      241 KHRIRRVLIYMDVYHGGTQFTPODPSVLFSTRHOGKRFWPLKASNMSTTFGGG 300
DB      241 KHRIRRVLIYMDVYHGGTQFTPODPSVLFSTRHOGKRFWPLKASNMSTTFGGG 300
QY      301 QGYTINVMNOYGMADADYIAAFLLVLPVLEFOPOLVLAAGFDALOGDPKGEAAATP 360
DB      301 QGYTINVMNOYGMADADYIAAFLLVLPVLEFOPOLVLAAGFDALOGDPKGEAAATP 360
QY      301 QGYTINVMNOYGMADADYIAAFLLVLPVLEFOPOLVLAAGFDALOGDPKGEAAATP 360
DB      301 QGYTINVMNOYGMADADYIAAFLLVLPVLEFOPOLVLAAGFDALOGDPKGEAAATP 360
QY      361 AGFAQLTHLMLAGLAKLILSLGGYNLRALAEVSAASHLTLGDPCEPMLESGAPCRSA 420
DB      361 AGFAQLTHLMLAGLAKLILSLGGYNLRALAEVSAASHLTLGDPCEPMLESGAPCRSA 420
QY      361 AGFAQLTHLMLAGLAKLILSLGGYNLRALAEVSAASHLTLGDPCEPMLESGAPCRSA 420
DB      361 AGFAQLTHLMLAGLAKLILSLGGYNLRALAEVSAASHLTLGDPCEPMLESGAPCRSA 420
QY      421 QASVSCALEALEPFEVLYRSTETVYERDMEDNVESEDEGPRWEPVLPILTWPYLSR 480
DB      421 QASVSCALEALEPFEVLYRSTETVYERDMEDNVESEDEGPRWEPVLPILTWPYLSR 480
QY      421 QASVSCALEALEPFEVLYRSTETVYERDMEDNVESEDEGPRWEPVLPILTWPYLSR 480
DB      421 QASVSCALEALEPFEVLYRSTETVYERDMEDNVESEDEGPRWEPVLPILTWPYLSR 480
QY      481 TGLVYDMMNHNCNMDSHHPEVPRILIRKLEELIAGAGCLTLTPPAEAEELTCH 540
DB      481 TGLVYDMMNHNCNMDSHHPEVPRILIRKLEELIAGAGCLTLTPPAEAEELTCH 540
QY      481 TGLVYDMMNHNCNMDSHHPEVPRILIRKLEELIAGAGCLTLTPPAEAEELTCH 540
DB      481 TGLVYDMMNHNCNMDSHHPEVPRILIRKLEELIAGAGCLTLTPPAEAEELTCH 540
QY      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSTFACQALATGAACRLVEAVLSEGVN 600
DB      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSTFACQALATGAACRLVEAVLSEGVN 600
QY      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSTFACQALATGAACRLVEAVLSEGVN 600
DB      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSTFACQALATGAACRLVEAVLSEGVN 600
QY      601 GAAYVPRPGHHAEDDACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGNTQHF 660
DB      601 GAAYVPRPGHHAEDDACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGNTQHF 660
QY      601 GAAYVPRPGHHAEDDACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGNTQHF 660
DB      601 GAAYVPRPGHHAEDDACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGNTQHF 660
QY      661 EDDSVLYVSLHRVDHGTFFPWGDGASQIGRAAGTGTVAVANNGPMDGADYLAANH 720
DB      661 EDDSVLYVSLHRVDHGTFFPWGDGASQIGRAAGTGTVAVANNGPMDGADYLAANH 720
QY      661 EDDSVLYVSLHRVDHGTFFPWGDGASQIGRAAGTGTVAVANNGPMDGADYLAANH 720
DB      661 EDDSVLYVSLHRVDHGTFFPWGDGASQIGRAAGTGTVAVANNGPMDGADYLAANH 720
QY      721 RLVPVIAEFNEPELVLSAGFDAAAGDPLGGGCVSPREGAHLTHLMLGASRIILILEG 780
DB      721 RLVPVIAEFNEPELVLSAGFDAAAGDPLGGGCVSPREGAHLTHLMLGASRIILILEG 780
```

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QY      781 GYNLTISSEMAACTRSILGDPPLTLPRPPLSGALASTETIYVRRRYRSIRYAKVE 840
DB      781 GYNLTISSEMAACTRSILGDPPLTLPRPPLSGALASTETIYVRRRYRSIRYAKVE 840
QY      841 DRGSPSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGOTNSET 900
DB      841 DRGSPSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGOTNSET 900
QY      841 DRGSPSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGOTNSET 900
DB      841 DRGSPSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGOTNSET 900
QY      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 960
DB      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 960
QY      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 960
DB      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 960
QY      961 ILDTTSEDAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 1020
DB      961 ILDTTSEDAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 1020
QY      961 ILDTTSEDAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 1020
DB      961 ILDTTSEDAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDOTTSEETVGA 1020
QY      1021 TPPLASSTHOTPTSPVQGTTPDISPTLIGSLRTLELSESGASQASQAPGENMLGEA 1080
DB      1021 TPPLASSTHOTPTSPVQGTTPDISPTLIGSLRTLELSESGASQASQAPGENMLGEA 1080
QY      1021 TPPLASSTHOTPTSPVQGTTPDISPTLIGSLRTLELSESGASQASQAPGENMLGEA 1080
DB      1021 TPPLASSTHOTPTSPVQGTTPDISPTLIGSLRTLELSESGASQASQAPGENMLGEA 1080
QY      1081 AGGQMDADSMLOGSRGLDQALFYAVTLPWCPRHLVAVCPIPAAGLDVTPQCGDCGTIQ 1140
DB      1081 AGGQMDADSMLOGSRGLDQALFYAVTLPWCPRHLVAVCPIPAAGLDVTPQCGDCGTIQ 1140
QY      1141 ENNVCLSCYGVYGGRYNGHMLQHNHSGHPRVLYSLDLSAMCYCCAYVHHQALLDVKN 1200
DB      1141 ENNVCLSCYGVYGGRYNGHMLQHNHSGHPRVLYSLDLSAMCYCCAYVHHQALLDVKN 1200
QY      1201 IAHQNKFGEDMPAPH 1215
DB      1201 IAHQNKFGEDMPAPH 1215

RESULT 5
US-09-976-280A-2
; Sequence 2, Application US/09976280A
; Patent No. US20020115177A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhimin
; TITLE OF INVENTION: Regulation of Human Histone Deacetylase
; FILE REFERENCE: 004974.00590
; CURRENT APPLICATION NUMBER: US/09/976,280A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,928
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-976-280A-2

Query Match      17.6%; Score 1125; DB 10; Length 673;
Best Local Similarity 37.2%; Pred. No. 5,4e-71;
Matches 283; Conservative 89; Mismatches 225; Indels 164; Gaps 20;

QY      85 GGTGLVDEDLNEFHCLMDSPF---EGPERLHAKEQLQELDLRCVSPQAREAEKE 140
DB      2 GATLVYHEDMTATRLIMDD--PCEETERPRLAIDLRLKORGLBQCLTSLAREASEE 59
QY      141 LMLVHSLEYIDLMETTYOANNEGELRYLADTYDSVYLHPSYSCACLAGSVLRVDAVLG 200
DB      60 LGLVHSPEVYSLVREHVGKELQALSQGFDAIFYHPSFHCARLAAGLQDLVDVAVLT 119
QY      201 AETRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQKHIRRVLLIVMDVHHNGGT 260
DB      120 GAVONGLALVPRPGHHCORAAANGFCVFNNVLAIAAHAKQKJELRILIVMDVHHNGGT 179
QY      261 QFTPODPSVLYFSHRYVQGRWPPLKASNMSTTFGGGCGTTINVMNOYGMADADYI 320
DB      180 QTLFEDPSVLYFSHRYVQGRWPPLKASNMSTTFGGGCGTTINVMNOYGMADADYI 239
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Query Match	12.6%	Score 805.5;	DB 9;	Length 1084;
Best Local Similarity	46.0%;	Pred. No. 4.1e-48;		
Matches 185;	Conservative 54;	Mismatches 118;	Indels 45;	Gaps 12

RESULT 9
US-10-173-539-12

Sequence 12, Application US/10173539
Publication No. US20030059912A1
GENERAL INFORMATION:
APPLICANT: Richon, Victoria
APPLICANT: Zhou, Xiabo
APPLICANT: Rikkind, Richard A.
APPLICANT: Marks, Paul A.
TITLE OF INVENTION: HNA9 Polypeptides and Polynucleotides
FILE REFERENCE: 3254.1000-003
CURRENT APPLICATION NUMBER: US/10/173,539
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/298,173
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/311,686

Query Match	12.6%	Score 805.5;	DB 9;	Length 1084;
Best Local Similarity	46.0%;	Pred. No. 4.1e-48;		
Matches 185; Conservative	54;	Mismatches 118;	Indels 45;	Gaps 12

RESULT 10
US-09-817-913-7

```

? Sequence 7, Application US/09817913
? Patent No. US20020061860A1
? GENERAL INFORMATION:
? APPLICANT: Li, Zuomei
? APPLICANT: Bonfills, Claire
? APPLICANT: Besterman, Jeffrey
? TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
? FILE REFERENCE: 106101.145
? CURRENT APPLICATION NUMBER: US/09/817,913
? CURRENT FILING DATE: 2001-03-26
? PRIOR APPLICATION NUMBER: US 60/192,157
? PRIOR FILING DATE: 2000-03-24
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 7
?
? LENGTH: 967
?
? TYPE: PRT
?
? ORGANISM: Human
?
? OS-09-817-913-7

```

[illegible]

QY 523 CTTLPREPATEALLTCHSAEYVGHILRAETKKTREHRE-----SSNF----- 566
 Db 581 CECIRGRKATLEELQTVHSEAH-T-LTYGNPLNRKLDKSKLLGLSLASFVRLPCGGVGV 639
 QY 567 --DSIYICPSTFACQALATGACRLVEAVLSEGVNLGAIVVRPGHHAEDDAACGFCFEN 624
 Db 640 DSDTIWNEVHSGAARLAVGVVELVFKVATGELKNGRVAVRPGHHAESTPMTGCTFN 699
 QY 625 SVAAVAARHAQ---TISGHALRILIVDMVHNHNGTQHMEDDPVLYVSLHRYDHGTFFP 681
 Db 700 SVAAVAARHAQ---TISGHALRILIVDMVHNHNGTQHMEDDPVLYVSLHRYDHGTFFP 755
 QY 682 MGDGASSQIGRAAGTGTFTVNAWNG---PRMGADYLAAMRVLPLATFERNPELVYS 738
 Db 756 --GSGAPDEVGTGPGGVNMAFTGGDPPMGDAEYLAARFTVMPPIASEFAPDVLAS 813
 QY 739 AGFDAARG--DPLGGCOVSPGEGYAHILTHLMGLASGRITLLEGGVNLTSISESMAACTR 796
 Db 814 SGFDAVEGHPTPLGGVNLASRCFGLTQKMLAGRLVLALEGGHDLTAICDASEACVS 873
 QY 797 SLIG---DPPLLTLPRPLSGALASITETIOVHRRYRSLR 835
 Db 874 ALLGNEIDPLPEKVLQQRPNANAVRSMKMEIHSKYRCLQ 915

RESULT 11

US-09-817-538-7
 ; Sequence 7, Application US/09817538
 ; Patent No. US20020137162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Zuomei
 ; APPLICANT: Bonfils, Claire
 ; APPLICANT: Besterman, Jeffrey
 ; TITLE OF INVENTION: Antisense oligonucleotide inhibition of Specific Histone
 ; FILE REFERENCE: 106101.144
 ; CURRENT APPLICATION NUMBER: US/09/817.538
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/192.157
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 967
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-817-538-7

Query Match 12.5%; Score 801.5; DB 10; Length 967;
 Best Local Similarity 45.8%; Pred. No. 6.6e-48;
 Matches 184; Conservative 54; Mismatches 119; Indels 45; Gaps 12;

QY 465 EPPVLPILTWPVLSRGVLYDQMANH-CNLM-DSHPEVPORILIMCRLEELGLGR 522
 Db 528 EPPKPRFT-----TGLVYDTLMLKHCQTCGSSSSHPHAGRIQSIIMSRLQETGRK 580
 QY 523 CTTLPREPATEALLTCHSAEYVGHILRAETKKTREHRE-----SSNF----- 566
 Db 581 CECIRGRKATLEELQTVHSEAH-T-LTYGNPLNRKLDKSKLLGLSLASFVRLPCGGVGV 639
 QY 567 --DSIYICPSTFACQALATGACRLVEAVLSEGVNLGAIVVRPGHHAEDDAACGFCFEN 624
 Db 640 DSDTIWNEVHSGAARLAVGVVELVFKVATGELKNGRVAVRPGHHAESTPMTGCTFN 699
 QY 625 SVAAVAARHAQ---TISGHALRILIVDMVHNHNGTQHMEDDPVLYVSLHRYDHGTFFP 681
 Db 700 SVAAVAARHAQ---TISGHALRILIVDMVHNHNGTQHMEDDPVLYVSLHRYDHGTFFP 755
 QY 682 MGDGASSQIGRAAGTGTFTVNAWNG---PRMGADYLAAMRVLPLATFERNPELVYS 738
 Db 756 --GSGAPDEVGTGPGGVNMAFTGGDPPMGDAEYLAARFTVMPPIASEFAPDVLAS 813

QY 739 AGFDAARG--DPLGGCOVSPGEGYAHILTHLMGLASGRITLLEGGVNLTSISESMAACTR 796
 Db 814 SGFDAVEGHPTPLGGVNLASRCFGLTQKMLAGRLVLALEGGHDLTAICDASEACVS 873
 QY 797 SLIG---DPPLLTLPRPLSGALASITETIOVHRRYRSLR 835
 Db 874 ALLGNEIDPLPEKVLQQRPNANAVRSMKMEIHSKYRCLQ 915

RESULT 12

US-10-072-094-6
 ; Sequence 6, Application US/10072094
 ; Publication No. US2003002538A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JACKSON, DONALD
 ; APPLICANT: LORENZI, MATTHEW
 ; APPLICANT: ATTAR, RICARDO
 ; APPLICANT: GOTTFARDS, MARCO
 ; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
 ; FILE REFERENCE: 3053-4145US1
 ; CURRENT APPLICATION NUMBER: US/10/072.094
 ; CURRENT FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 60/298.296
 ; PRIOR FILING DATE: 2001-06-14
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 706
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-10-072-094-6

Query Match 12.3%; Score 788; DB 9; Length 706;
 Best Local Similarity 35.4%; Pred. No. 3.7e-47;
 Matches 180; Conservative 90; Mismatches 190; Indels 48; Gaps 12;

QY 436 EYLVRSSTETVER---DNMEEDNVESEEGPWE---PVPVLPILTWPVLSRGVLYDQNM 489
 Db 9 EYLVENDHDLKRLKENKEBENSLSSTSKSRQVIVPCMKIHYSP-L-KTGICVYRM 66
 QY 490 MNHCNIMDSH-----HPEVPORILIMCRLEELG-----LAGRCITLTPRPA 531
 Db 67 RYHAKITFTYFEYIDHPEDPRIRIYKILANGILNPTLSGVLDGLMLKIPYRAA 126
 QY 532 TEAEILTCHSAEYVGHILRAETKKTREHRESNPDSIYICPSTFACQALATGACACTE 591
 Db 127 TSEELLEVHTKELEFTESTEKMSREELKETEKGDSVYFNDSYASARLPCGGAIEACK 186
 QY 592 AVLSGEVNLGAIVVRPGHHAEDDAACGFCFENSVAVAARH-AOTISGHALRILIVDMV 650
 Db 187 AVYEGSVKNSLAVVRPGHHAEPQAAGGFCLESNVAANKIILKNPESYRRLIMLMDI 246
 QY 651 HHNGTQHMEDDPVLYVSLHRYDHGTFFPMGDEGASSQIGRAAGTGTFTVNAWNGPRM 710
 Db 247 HHNGTQKSFYQDDQVLYVSLHREFGKTYPGTIGQYDQDTGSGKGFGFNCNITWPGV 306
 QY 711 GPADYLAAMRVLPLATFERNPELVYSAGFDAARDPLAGGCOVSPGEGYAHILTHLMGLA 770
 Db 307 GDAEYMAAEQVYMPGREFKPDVLISSGFGDAADDITIGQCHVTSPSCGHNHMLKSLA 366
 QY 771 SGRIILILEGGVNLTSISESMAACTRSILGDDPPLTLPRP---PLSGALASTETIOVH 827
 Db 367 RGNLCVLEGGVNLTAIAIASLAVKYLIGEPD--ELDPDLSDPREYEMIDKYLRLQ 424
 QY 828 RRYWSRLRYMKE---DREGPSSSKLVTKKAPAPKRLAERMTTREKKVLEAGMGKVT- 883
 Db 425 SKYWCFCRRRHAHNSGCFNEPINDSIISKNF-----LQKAIHQOQHYLSOEFNVTIL 478
 QY 884 ---SASFGEES---TPGQJNSETAVVAL 905
 Db 479 PLVSMDLDPNTVLCTPNISESNTIIVV 506

Query Match	12.2%	Score 778.5;	DB 9;	Length 716;
Best Local Similarity	37.1%	Pred. No. 1.8e-46;		
Matches 192;	Conservative 79;	Mismatches 179;	Indels 67;	Gaps 16

RESULT 14
US-10-072-094-8
Sequence 8, Application US/10072094
Publication No. US20030025538A1
GENERAL INFORMATION:
APPLICANT: JACKSON, DONALD
APPLICANT: LORENZI, MATTHEW
APPLICANT: ATTAR, RICARDO
APPLICANT: GOTTARDIS, MARCO
TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES

Query Match	12.2%	Score 778.5	DB 9	Length 1122
Best Local Similarity	37.1%	Pred. No. 3.5e-46		
Matches 192, Conservative	79	Mismatches 179	Indels 67	Gaps 16

```

RESULT 15
US-10-072-094-91
: Sequence 91, Application US/10072094
: Publication No. US20030025538A1
: GENERAL INFORMATION:
: APPLICANT: JACKSON, DONALD
: APPLICANT: LORENZI, MATTHEW
: APPLICANT: ATTAR, RICARDO
: APPLICANT: GOTTARDIS, MARCO
: TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
: FILE REFERENCE: 3053-41450S1
: CURRENT APPLICATION NUMBER: US/10/072,094
: CURRENT FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: 60/298,296
: PRIOR FILING DATE: 2001-06-14
: NUMBER OF SEQ ID NOS: 127
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 91
: LENGTH: 1122

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-094-91

Query Match 12.2%; Score 778.5; DB 9; Length 1122;
Best Local Similarity 37.1%; Pred. No. 3.5e-46;
Matches 192; Conservative 79; Mismatches 179; Indels 67; Gaps 16;

```
QY 408 PMLESPAGPCSAQASVSCALELEFEWEVLYRSTETVERDNMEDNVESEEGPWEP 467
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 617 PDLEEPGAGYKKLPDQ-PLQPLQVYQAPL-SLATVPHQATGTOSSPAAGCKSP 673
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 468 VLPI--LTPRVLSRTGLVYDQMMNH-CNLMDSH-HPEVQRILRMCRLEELAGR 522
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 674 DQPKHLEF-----TGVDITPMLKHQCMGNTVHPEHAGRIQSIWSRLQETGLSK 726
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 523 CLFLTPPATEALLTCHSAEYVGHRLATEKMTREHRE-----S 563
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 727 CERIRGRKATLDEIQTVHS-EYHILYGTSPLNROKLDCKLGPISQMYAVLPQGGIG 785
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 564 SNEDSIITICPSTFACQALATGACRLVEAVLSGEVLNGAAVRRPGHHAQDACGCF 623
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 786 VDSDTVNMENHSSAVMAVGCLELFAKVAAGELKNGFALIRPGHHAESTAMGFCFF 845
    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 624 NSVAVARHMQTISGHALRIIYMDVHNGTQHMEDDPSVLYSLHRIDHGTFFPMG 683
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 846 NSVAITAKLLQO-KLVNGKVLIVMDIHNGTQOAFYNDPSVLYSLHRYDNGNFP-- 902
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 684 DEGASSQIGRAAGTFTVNVAMNG--PRMGADYLAAMHRLVLPVAYEFPDELTVSAG 740
    || : : | : | : | : | : | : | : | : | : | : | : | : | :
Db 903 GSGAPEEVGGPGVGVNVNVAMTGVDPIDGVEYLTAFRTVMPFAHESPDVVLVSAG 962
    || : : | : | : | : | : | : | : | : | : | : | : | : | :
QY 741 FDAARG--DPLGGQVSPEGYAHLTFLMLGLASGRILLLEGYNLTSSISMAACTRSL 798
    ||| | : : | : | : | : | : | : | : | : | : | : | : | : |
Db 963 FDAVEGHLSPLGYSYARCGHLTRQMLTAGGRVYALLEGHDLFALCDASEACYSAL 1022
    ||| | : : | : | : | : | : | : | : | : | : | : | : | : |
QY 799 LG---DPPPLTLPRPLSGALASITETIOVHRRW-----RSLR---VMKYED 841
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1023 LSYELOPLDEAVLQOKPRINAVATLEKVIETIOSKHWSCVQKFAAGLGRLEAQAGETEE 1082
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 842 REGPSSSKLVYKKAPPA-----KPLAERMTTRE 871
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1083 AETVSNMALLSVGAEOQAAAAAARHSPRAPEPMEOE 1119
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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Search completed: June 6, 2003, 14:58:56
Job time : 59 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 16:37:51 ; Search time 752 Seconds
(without alignments)
10924.588 Million cell updates/sec

Title: US-09-800-187-5

Perfect score: 3648
Sequence: 1 atgacctcaacgcgcagga.....atagcccccacacactaa 3648

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
N.Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
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18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3646.4	100.0	6949	24	AAS95017	Human DNA sequence
2	3612.4	99.0	4099	24	ABR87720	Human CDNA encodin
3	2282	62.6	2552	22	AAH18350	Human CDNA sequenc
4	2182.6	59.8	2548	22	AAH14416	Human CDNA sequenc
5	1398.8	38.3	2107	21	AAC59704	Human secreted pro
6	628.2	17.2	638	22	AAH06343	Human CDNA clone (
7	602.2	16.5	743	22	AAH03528	Human CDNA clone (
8	453.2	12.4	4689	23	ABH10649	Drosophila melanog
9	398.4	10.9	424	20	AAV87399	EST clone CD146.

10	347.6	9.5	2461	21	AAC76966	Human ORFX ORF2521
11	346	9.5	2022	24	ABO73028	Human HDAC9 encodi
12	346	9.5	2022	24	AAH36979	Human histone deac
13	346	9.5	2104	24	ABO73030	Human HDAC9 varian
14	346	9.5	2480	21	AAC76952	Human ORFX ORF2507
15	325.8	8.9	1005	22	AAH41280	CDNA encoding nove
16	300.6	8.2	9384	23	ABH10648	Drosophila melanog
17	289.8	7.9	1129	24	ABO73027	Human HDAC9 ORF nu
18	278.2	7.6	744	24	ABO73013	Human HDAC9 relate
19	235.4	6.5	2621	21	AAH81740	Human secreted pro
20	229.6	6.3	1875	21	ABO73031	Human HDAC9 varian
21	215.4	5.9	1725	21	AAH51856	Caspase 8-Interact
22	215.4	5.9	4200	22	AAK53008	Human polyomucleot
23	215.4	5.9	4245	22	AAK53024	Human polyomucleot
24	215	5.9	2430	22	ABH90159	Human CDNA sequenc
25	213.8	5.9	3208	22	AAH14008	Human ORFX ORF2609
26	213.8	5.9	4189	21	AAH77054	Human CDNA encodin
27	208.6	5.7	3131	24	ABH87721	Human CDNA sequenc
28	204.4	5.6	2026	22	AAH13829	Human CDNA encodin
29	201	5.5	606	22	AAH03697	Human CDNA clone (
30	194	5.3	8459	22	AAC89557	Human histone deac
31	192.4	5.3	8460	22	ABH87718	Human CDNA encodin
32	175.2	4.8	4021	21	AAH7217	Human ORFX ORF2772
33	173.6	4.8	2233	22	AAC89558	Human histone deac
34	173.6	4.8	2233	22	ABH87719	Human CDNA encodin
35	173.6	4.8	2885	20	AAH40055	Human CDNA encodin
36	170.8	4.7	2205	24	ABO73029	Human cancer assoc
37	165.8	4.5	1355	24	ABH34632	Human HDAC9 relate
38	163	4.5	719	22	AAH07464	Human CDNA for nov
39	161.4	4.4	1880	22	AAH16517	Human CDNA clone (
40	160.8	4.4	843	24	ABO73009	Human CDNA sequenc
41	158	4.3	3894	23	ABH03353	Human CDNA relate
42	142	3.9	560	22	AAH1402	Drosophila melanog
43	140.4	3.8	1452	22	AAH62798	Human CDNA clone (
44	139.6	3.8	631	24	ABO73018	Human HDAC9 relate
45	139.2	3.8	1991	21	AAC34680	Arabidopsis thailia

ALIGNMENTS

RESULT 1	AAS95017/c	standard; DNA: 6949 BP.
ID	AAS95017	
AC	AAS95017	
DT	14-FEB-2002	(first entry)
XX	Human DNA sequence #272 expressed during foam cell differentiation.	
DE	Human; foam cell differentiation; atherosclerosis; cerebral stroke;	
KW	Cardiovascular disorder; coronary artery disease; gene therapy; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200177389-A2.	
XX		
PD	18-OCT-2001.	
XX		
PF	04-APR-2001; 2001WO-US11128.	
XX		
PR	05-APR-2000; 2000US-195106P.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
XX		
PI	Shiffman D, Somogyi R, Lawn R, Sellhammer JJ, Porter GJ, Miki T;	
PI	Tal J;	
XX		
XX	WPI; 2002-010925/01.	
XX		
PT	Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that	

PT are differentially expressed in foam cell development -

XX Claim 1, page 311-313; 315pp; English.

XX The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used
CC as PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. AAS94746-AAS95021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation.

XX Sequence 6949 BP; 1468 A; 2002 C; 1934 G; 1542 T; 3 other;

Query Match 100.0%; Score 3646.4; DB 24; Length 6949;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

YY 1 ATGACCTCAACCGCGCCAGATTCACCAACAGGAGGAGAGATAGGACAGACCCC 60
DB 6819 ATATCTTCACACCGCGCCAGATTCACCAACAGGAGGAGAGATAGGACAGACCCC 6760
YY 61 CAGTCGCCCTCAGAGACTCAGATGTCACCTCGAAGGAAATATTAAGGAGCCGTT 120
DB 6759 CAGTCGCCCTCAGAGACTCAGATGTCACCTCGAAGGAAATATTAAGGAGCCGTT 6760
YY 121 CCCCCGCTATCCCAATCTAGGAGGAGTAAAGAAAGGCAATAGAAAGCTGGC 180
DB 6699 CCCCCGCTATCCCAATCTAGGAGGAGTAAAGAAAGGCAATAGAAAGCTGGC 6640
YY 181 CAAGCAATGGAAGAAGACTATATCTGAGGACTGCAAGGATGATGAACTTGAAGCT 240
DB 6639 CAAGCAATGGAAGAAGACTATATCTGAGGACTGCAAGGATGATGAACTTGAAGCT 6580
YY 241 GAAAGCACTGGCTGGACATGGCTTGGTGGATGAGAGGTTAAATGAATTCATTCGCTC 300
DB 6579 GAAAGCACTGGCTGGACATGGCTTGGTGGATGAGAGGTTAAATGAATTCATTCGCTC 6520
YY 301 TGGGATGACAGCTTCCCGAAGGCCCTGAGCGGCTCATGCTCAAGAGCAACTGATC 360
DB 6519 TGGGATGACAGCTTCCCGAAGGCCCTGAGCGGCTCATGCTCAAGAGCAACTGATC 6460
YY 361 CAGAGAGGCTCTCAGATGCTGGTGGTCTTTCAGGCCGGTTTGGTGAAGAAAGAGAG 420
DB 6459 CAGAGAGGCTCTCAGATGCTGGTGGTCTTTCAGGCCGGTTTGGTGAAGAAAGAGAG 6400
YY 421 CTGATGTTGGTTCACAGCTAGATATATATGATCTGATGAAACACCACTAGATGAT 480
DB 6399 CTGATGTTGGTTCACAGCTAGATATATATGATCTGATGAAACACCACTAGATGAT 6340
YY 481 GAGGAGAACTCCGTGCTAGACAGACACTAGACTCAAGTTATCTGATCCGAACTCA 540
DB 6339 GAGGAGAACTCCGTGCTAGACAGACACTAGACTCAAGTTATCTGATCCGAACTCA 6280
YY 541 TACTCGTGTGCTGGCTGGCTCAGGCTGCTGCTCAGGGTGGGATGGGCTCTGGGG 600
DB 6279 TACTCGTGTGCTGGCTGGCTCAGGCTGCTGCTCAGGGTGGGATGGGCTCTGGGG 6220
YY 601 GCTGAGATCCGGAATGAGCATGGCCATTAAGGCTCTGAGACATCAAGCCACAGACAGT 660
DB 6219 GCTGAGATCCGGAATGAGCATGGCCATTAAGGCTCTGAGACATCAAGCCACAGACAGT 6160
YY 661 CTATGATGATGCTATGATGATGATCAACAGAGTGGCTGTGGAGCCGCTATGCTCAACAG 720
DB 6159 CTATGATGATGCTATGATGATGATCAACAGAGTGGCTGTGGAGCCGCTATGCTCAACAG 6100
YY 721 AAACACCGCATCCGAGAGGCTCTTATCTGATGATGGATGTGACACAGGCTCAAGAA 780

DB 6099 AAACACCGCATCCGAGAGGCTCTTATCTGATGATGGATGTGACACAGGCTCAAGAA 6040
YY 781 CAGTTACACTTCGACAGAGACCCAGATGCTCTATTTCTCATCCACCGCTACAGAGAG 840
DB 6039 CAGTTACACTTCGACAGAGACCCAGATGCTCTATTTCTCATCCACCGCTACAGAGAG 5980
YY 841 GGTAGGTTTCGGCCCAAGGCTCTAAGGCTCTAAGGCTCTAAGGCTCTAAGGCTCTAAGG 900
DB 5979 GGTAGGTTTCGGCCCAAGGCTCTAAGGCTCTAAGGCTCTAAGGCTCTAAGGCTCTAAGG 5920
YY 901 CAAGATATATCAATCAATATGCTCTTGAACAGAGGAGGATGCGGATGCTGATACAT 960
DB 5919 CAAGATATATCAATCAATATGCTCTTGAACAGAGGAGGATGCGGATGCTGATACAT 5860
YY 961 GCTGCTTTCTGACAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 5859 GCTGCTTTCTGACAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5800
YY 1021 GTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 5799 GTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5740
YY 1081 GCAGGGTTCGCCAGCTAACCCACCTGCTCATGGGCTGCGCAGAGAGCAAGCTGATCCTG 1140
DB 5739 GCAGGGTTCGCCAGCTAACCCACCTGCTCATGGGCTGCGCAGAGAGCAAGCTGATCCTG 5680
YY 1141 TCTCTGAGAGGCTGCTACACCTCCGCGCCCTGCTGCTGAGAGGCTGATGCTGCTCAG 1200
DB 5679 TCTCTGAGAGGCTGCTACACCTCCGCGCCCTGCTGCTGAGAGGCTGATGCTGCTCAG 5620
YY 1201 ACCCTTCGGAGAGCCCTTGGCCCATGCTGAGTACCTGATGCTGCTGCTGCTGCTGCTG 1260
DB 5619 ACCCTTCGGAGAGCCCTTGGCCCATGCTGAGTACCTGATGCTGCTGCTGCTGCTGCTG 5560
YY 1261 CAGGCTTCAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 5559 CAGGCTTCAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5500
YY 1321 TCAACTGAGACCTGAGAGAGGAGACATGAGAGAGAGCAATGATGAGAGAGAGAGAG 1380
DB 5499 TCAACTGAGACCTGAGAGAGGAGACATGAGAGAGAGCAATGATGAGAGAGAGAGAG 5440
YY 1381 GAAAGACCTTGGAGAGCCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 5439 GAAAGACCTTGGAGAGCCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5380
YY 1441 ACAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 5379 ACAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5320
YY 1501 CCTGAGGTTACCCAGCGCATCTTGGGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 5319 CCTGAGGTTACCCAGCGCATCTTGGGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5260
YY 1561 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
DB 5359 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5200
YY 1621 AGTCTGAGTACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 5199 AGTCTGAGTACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5140
YY 1681 CGTGAGAGTTCCAACTTGAATCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
DB 5139 CGTGAGAGTTCCAACTTGAATCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5080
YY 1741 CTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
DB 5079 CTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5020
YY 1801 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860

FT FT [trans]_except- (pos:1255..1257,aa:11e) /trans]_except- (pos:1321..1323,aa:11e)
FT FT /trans]_except- (pos:1513..1515,aa:11e) /trans]_except- (pos:1627..1629,aa:11e)
FT FT /note= "Xaa is represented as an O in the specification"
FT FT /trans]_except- (pos:1648..1650,aa:11e)
FT FT /trans]_except- (pos:1669..1671,aa:11e)
FT FT /trans]_except- (pos:1834..1836,aa:11e)
FT FT /trans]_except- (pos:1873..1875,aa:11e)
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FT FT /trans]_except- (pos:1954..1956,aa:Cys)
FT FT /trans]_except- (pos:2485..2487,aa:11e)
FT FT /trans]_except- (pos:2608..2610,aa:Val)
FT FT /trans]_except- (pos:2809..2811,aa:Cys)
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FT FT /trans]_except- (pos:3277..3279,aa:Ser)
FT FT /trans]_except- (pos:3322..3324,aa:Leu)
FT FT /trans]_except- (pos:3367..3369,aa:Met)
FT FT /trans]_except- (pos:3439..3441,aa:Leu)
FT FT /trans]_except- (pos:3550..3552,aa:Cys)
FT FT /trans]_except- (pos:3619..3621,aa:Tyr)
FT FT /trans]_except- (pos:3640..3642,aa:Cys)
modified_base 1513
FT FT /tag= b
FT FT /mod_base= OTHER
FT FT /note= "Represented as an L in the specification"
PN PN US2002061860-A1.
XX XX 23-MAR-2002.
PR PR 06-AUG-2001; 2001US-0817913.
XX XX 24-MAR-2000; 2000US-192157P.
XX XX (L1R2/) LI Z.
PA (BOUF/) BONFILS C.
PA (BEST/) BESTERMAN J.
XX XX
PI L1 Z, Bonfills C, Besterman J;
XX XX
DR WPI: 2002-507650/54.
XX P-PSDB; AAU99661.
XX
PS Claim 6; Fig 6B; 60pp; English.
XX
CC The invention relates to an agent that inhibits an isoform of histone
CC deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an
CC antisense oligonucleotide. Also included are inhibiting an HDAC isoform
CC in a cell by treatment with the agent, identifying an HDAC isoform that
CC is required for induction of cell proliferation or differentiation and
CC inhibiting cell proliferation by treatment with two antisense
CC oligonucleotides or small molecules that inhibit a specific HDAC
CC isoform, or antisense oligonucleotide or small molecules that inhibit
CC DNA methyltransferase. The agent therefore acts as a tumour suppressor.
CC The agents are used to treat diseases of cell proliferation and
CC differentiation (e.g. cancer and tumours), by inducing growth retardation,
CC growth arrest or programmed/necrotic cell death, specifically neoplastic
CC cell proliferation in humans. The agents are selective for particular
CC isoforms, compared to known inhibitors which are not selective.
CC The present sequence encodes the HDAC-6 isoform.
XX
SO Sequence 4099 BP; 904 A; 1221 C; 1168 G; 804 T; 2 other;
Query Match 99.0%; Score 3612.4; DB 24; Length 4099;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3625; Conservative 0; Mismatches 23; Indels 0; Gaps 0

Db	94	ATGACCTCAACCGGCGAGAAATTCACCAACCAACGAGCGAAGAAATAGGCAGAACCC	153
Qy	61	CAGTGGCCCCCTCAGAGACTCCAGTGTCACTTCGAAAGCCAAATATTTAAAAGAGGCC	120
Db	154	CAGTGGCCCCCTCAGAGACTCCAGTGTCACTTCGAAAGCCAAATATTTAAAAGAGGCC	213
Qy	121	CCCCCTCTATCCCAATCTAGCGGAGGTAAAGAAAGCAAAATGACAGAGCTCGGC	180
Db	214	CCCCCTCTATCCCAATCTAGCGGAGGTAAAGAAAGCAAAATGACAGAGCTCGGC	273
Qy	181	CAAGCAATGGAAGAAGACCTTAATCGTGGAGATGCAAGGATGATCTGAACCTTGAGCT	240
Db	274	CAAGCAATGGAAGAAGACCTTAATCGTGGAGATGCAAGGATGATCTGAACCTTGAGCT	333
Qy	241	GAAAGACTGGGTGGGACTGCGCTTGGTGTGGATGAGCGATTAAATGAATTCATTGCTC	300
Db	334	GAAAGACTGGGTGGGACTGCGCTTGGTGTGGATGAGCGATTAAATGAATTCATTGCTC	393
Qy	301	TGCGATGACACTTCCCGGAAGGCGCTTAGGCGGCTCAATGCCATCAGAGCAACTGATC	360
Db	394	TGCGATGACACTTCCCGGAAGGCGCTTAGGCGGCTCAATGCCATCAGAGCAACTGATC	453
Qy	361	CAGGAGGGCTCTAGATGCTGCTGCTCTTTCAAGGCCGCGTTTGTGAAAAGGAAG	420
Db	454	CAGGAGGGCTCTAGATGCTGCTGCTCTTTCAAGGCCGCGTTTGTGAAAAGGAAG	513
Qy	421	CTGATGTTGGTTCACAGCCTAGAAATATTTATCTGATGGAACAACCCACTACTGAT	480
Db	514	CTGATGTTGGTTCACAGCCTAGAAATATTTATCTGATGGAACAACCCACTACTGAT	573
Qy	481	GAGGAGAACTCCGCTGTCTAGACAGACACTACGACTAGTTTATCTGATCCGAATCA	540
Db	574	GAGGAGAACTCCGCTGTCTAGACAGACACTACGACTAGTTTATCTGATCCGAATCA	633
Qy	541	TACTCTGTGCTGCTGCTGAGGCTCTGTCTCAGGCTGTGGATGCGGTCTTGAGG	600
Db	634	TACTCTGTGCTGCTGCTGAGGCTCTGTCTCAGGCTGTGGATGCGGTCTTGAGG	693
Qy	601	GCTGAGATCCCGAATNGCATGCCATCATTTAGGCGCTCTGGAACATCAGCCCAACAGT	660
Db	694	GCTGAGATCCCGAATNGCATGCCATCATTTAGGCGCTCTGGAACATCAGCCCAACAGT	753
Qy	661	CTTATGATGAGCTATTTGCATGTTCAACACAGTGGCTGTGGAGCCGCTATGCTCAAG	720
Db	754	CTTATGATGAGCTATTTGCATGTTCAACACAGTGGCTGTGGAGCCGCTATGCTCAAG	813
Qy	721	AAACACGCGATCCGAGGGGCTCTATGCTAGATTGGATGTGCAACACGCTCAAGAACA	780
Db	814	AAACACGCGATCCGAGGGGCTCTATGCTAGATTGGATGTGCAACACGCTCAAGAACA	873
Qy	781	CAGTTCACTCTGACACAGACCCCAAGTGTCTCTATTTCTCATTCACACGCTACAGAG	840
Db	874	CAGTTCACTCTGACACAGACCCCAAGTGTCTCTATTTCTCATTCACACGCTACAGAG	933
Qy	841	GGTAGGTTCTGGGCCACAGTGAAGGCTCTAACTGATGCACACAGGTTTGGCCAAAGC	900
Db	934	GGTAGGTTCTGGGCCACAGTGAAGGCTCTAACTGATGCACACAGGTTTGGCCAAAGC	993
Qy	901	CAAGGATATACCATCAATGTGCTTTGGAACACAGGTGGGAGTGGGATGCTGACTACAT	960
Db	994	CAAGGATATACCATCAATGTGCTTTGGAACACAGGTGGGAGTGGGATGCTGACTACAT	1053
Qy	961	GCTGCTTTCCGACAGCTGCTGCTGCGCAATGCCCTCCAGTTCCAGCCTCAGTGGTCTG	1020
Db	1054	GCTGCTTTCCGACAGCTGCTGCTGCGCAATGCCCTCCAGTTCCAGCCTCAGTGGTCTG	1113
Qy	1021	GTGCTGCTGATTTGATGCCCTCAGAGGGAACCCAAAGGTTGATGAGCGGCACATCCG	1080
Db	1114	GTGCTGCTGATTTGATGCCCTCAGAGGGAACCCAAAGGTTGATGAGCGGCACATCCG	1173
Qy	1081	GCAGGGTTGCGCCAGCTAACCCACCTGCTCATGGGCTGCGCAGAGGCAAGCTGATCTG	1140

Db 1174 GAAAGGTTGGCCAGCTAACCCACTGCTCATGGGTCGTGCAGAGGCAAGCTGATCTG 1233
 Qy 1141 TCTCTGAGAGGTGGTACAAACCTCCGGGCGCTGGTGAAGGCGTCACTGCTGCTCCAC 1200
 Db 1234 TCTCTGAGAGGTGGTACAAACCTCCGGGCGCTGGTGAAGGCGTCACTGCTGCTCCAC 1293
 Qy 1201 ACCCTTCTGGAGAGACCTTGGCCCATGCTGAGTCACTGGTGGCCCTCCGGAGTGGC 1260
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 Qy 1261 CAGGCTTCAAGTTCTCTGCTGTGAAGCCCTTGAGCCCTTCTGGAGGTTCTTGTGAGA 1320
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 Db 1714 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773
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 Db 1774 GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833
 Qy 1741 CTGTCACATGGGCGCTGCG 1800
 Db 1834 CTGTCACATGGGCGCTGCG 1893
 Qy 1801 GGTGCTGT 1860
 Db 1894 GGTGCTGT 1953
 Qy 1861 TGTCTTTTCACTGT 1920
 Db 1954 NGCTTTTCACTGT 2013
 Qy 1921 CTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Db 2014 CTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2073
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 Db 2074 GAGGATGAGCCCACTGT 2133
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 Db 2134 CCCATGGGGGATGAGGGGTGCCAGACAGATCGGGCGGGTGCAGGGGCAAGGCTTCCAC 2193
 Qy 2101 GTCAACGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Db 2194 GTCAACGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2253
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 Db 2254 GCGCTGT 2313

Qy 2221 TTTGATGCTGTACCGGGGGGATCCGCTGGGGGGCTGCCAGGTGTCACTGAGGGTTATGCC 2280
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 Qy 2281 CACCTCACCACTGCTGATGGGCTTGCAGTGGGCCCATTTATCTTATCTTATAGAGGT 2340
 Db 2374 CACCTCACCACTGCTGATGGGCTTGCAGTGGGCCCATTTATCTTATCTTATAGAGGT 2433
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      |||
Db 880 CAGTTCACCTTTCACAGAGACCCCAAGTCTGCTCAATTTCTCCATCCACGCGTACAGAG 939
QY 841 GGTAGGTTCTGGGCCCCACCTGAAAGCCCTTAACGTGTCCACACAGGTTTGCCCAAGGC 900
      |||
Db 940 GGTAGGTTCTGGGCCCCACCTGAAAGCCCTTAACGTGTCCACACAGGTTTGCCCAAGGC 999
QY 901 CAAGGATATACATCAATATGTCCTTGGAAACAGGTGGGATGCGGATGCTGACTACAT 960
      |||
Db 1000 CAAGGATATACATCAATATGTCCTTGGAAACAGGTGGGATGCGGATGCTGACTACAT 1059
QY 961 GCTGCTTCTCCGACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
      |||
Db 1060 GCTGCTTCTCCGACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
QY 1021 GTGGCTGCTGATTTGATGTCCTGCAAGGGGACCCCAAGGGTGAATGTCGCCACTCCG 1080
      |||
Db 1120 GTGGCTGCTGATTTGATGTCCTGCAAGGGGACCCCAAGGGTGAATGTCGCCACTCCG 1179
QY 1081 GCAGGGTTCGCCACAGCTAACCCACCTGCTCATGGGTGTGGCAGAGGCAAGCTGATCTG 1140
      |||
Db 1180 GCAGGGTTCGCCACAGCTAACCCACCTGCTCATGGGTGTGGCAGAGGCAAGCTGATCTG 1239
QY 1141 TCTCTGAGAGGGTGGCTAACACCTCCGGCCCTGGCTGTAAGGCTGCTGCTGCTGCTG 1200
      |||
Db 1240 TCTCTGAGAGGGTGGCTAACACCTCCGGCCCTGGCTGTAAGGCTGCTGCTGCTGCTG 1299
QY 1201 ACCCTTCTGGAGAGACCTTGCCTCCCATGCTGAGTACATGGTGGCCCTGCGGAGTGC 1260
      |||
Db 1300 ACCCTTCTGGAGAGACCTTGCCTCCCATGCTGAGTACATGGTGGCCCTGCGGAGTGC 1359
QY 1261 CAGGCTTCACTTCTGCTGCTGGAAGCCCTTGAGCCCTTCTGGAAGGTTCTTGTAGA 1320
      |||
Db 1360 CAGGCTTCACTTCTGCTGCTGGAAGCCCTTGAGCCCTTCTGGAAGGTTCTTGTAGA 1419
QY 1321 TCACCTGAGACCGTGGAGAGGAGACACATGAGAGAGACAAATGTAGAAGAGCGAGAG 1380
      |||
Db 1420 TCACCTGAGACCGTGGAGAGGAGACACATGAGAGAGACAAATGTAGAAGAGCGAGAG 1479
QY 1381 GAAGAGCCCTGGAGAGCCCTGCTGCTCCCAATCTGACATGAGGCGTACATCTCCG 1440
      |||
Db 1480 GAAGAGCCCTGGAGAGCCCTGCTGCTCCCAATCTGACATGAGGCGTACATCTCCG 1539
QY 1441 ACAGGGCTGCTCATGACCAAAATATGATGATCACTGCAACTGTGGACAGCCACCAC 1500
      |||
Db 1540 ACAGGGCTGCTCATGACCAAAATATGATGATCACTGCAACTGTGGACAGCCACCAC 1599
QY 1501 CCTGAGAGTACCCACAGCGCATCTTGGCGATCATGTGCCGTGGAAGCTGGGCCCTTGC 1560
      |||
Db 1600 CCTGAGAGTACCCACAGCGCATCTTGGCGATCATGTGCCGTGGAAGCTGGGCCCTTGC 1659
QY 1561 GGGCGCTGCTCACCCTGACAGCGCGCCCTGACAGAGGCTGAGTGTCTCACTGTCCAC 1620
      |||
Db 1660 GGGCGCTGCTCACCCTGACAGCGCGCCCTGACAGAGGCTGAGTGTCTCACTGTCCAC 1719
QY 1621 AGTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
      |||
Db 1720 AGTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1779
QY 1681 CGTGAAGATTCCAACTTGTACTCATCTATATCTGCCCCAGTACCTTGGCTGTGCACAG 1740
      |||
Db 1780 CGTGAAGATTCCAACTTGTACTCATCTATATCTGCCCCAGTACCTTGGCTGTGCACAG 1839
QY 1741 CTTGCACTGGGCGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
      |||
Db 1840 CTTGCACTGGGCGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899
QY 1801 GGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
      |||
Db 1900 GGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1959
QY 1861 TGCCTTTTCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
```

```
Db 1960 TGCCTTTTCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2019
QY 1921 CTACGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
      |||
Db 2020 CTACGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2079
QY 1981 GAGATGACCCCAAGTGTCTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
      |||
Db 2080 GAGATGACCCCAAGTGTCTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2139
QY 2041 CCCATGGGGGATGAGGGTGCACAGCCAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
      |||
Db 2140 CCCATGGGGGATGAGGGTGCACAGCCAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2199
QY 2101 GTCAACGTGGCATGAGAGGGGCCCGCATGGGTGATGCTGATGCTGATGCTGATGCTG 2160
      |||
Db 2200 GTCAACGTGGCATGAGAGGGGCCCGCATGGGTGATGCTGATGCTGATGCTGATGCTG 2259
QY 2161 CGCCTGTGTCTTCCCATTTGCTTACAGATTTTAAACCAAACTGTGTGTGTGTGTGTGTGT 2220
      |||
Db 2260 CGCCTGTGTCTTCCCATTTGCTTACAGATTTTAAACCAAACTGTGTGTGTGTGTGTGTGT 2319
QY 2221 TTTGATGCTGACAGGGGGGATCCGCTGGGGGGCTGCAAGGTGTACCTGAGGTTATGCC 2280
      |||
Db 2320 TTTGATGCTGACAGGGGGGATCCGCTGGGGGGCTGCAAGGTGTACCTGAGGTTATGCC 2379
QY 2281 CACCTCAACCC 2290
      |||
Db 2380 CACCTCAACCC 2389
      |||

RESULT 4
AAH14416
ID AAH14416 standard; cDNA: 2548 bp.
XX
AC AAH14416;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:11863.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
XX
PR 27-AUG-1999; 99JP-0300253.
XX
PR 11-JAN-2000; 2000JP-0118776.
XX
PR 02-MAY-2000; 2000JP-0183767.
XX
PR 09-JUN-2000; 2000JP-0241899.
XX
FA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI: 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 11863; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
```


Db	535	CACCAACCTGGCTGACC - TGGCAGGCCCCACACTATCAGGAGGCCCTGGCTTCATCTACGTGA	592
OY	2466	GACCAATCCAAAGTCCATCGCAGATACCTACCTGCGCAGCTTACGGTTCATGAAAGTGAAGACAG	2525
Db	593	GACCAATCCAAAGTCCATCGCAGATACCTGCGCAGCTTACGGTTCATGAAAGTGAAGACAG	652
OY	2526	AGAAAGACCCTCCAGTTCTAAGTTGGTCCACAAAGAAAGGACCCCAACCAAGCCCAACCTCAG	2588
Db	653	AGAAAGACCCTCCAGTTCTAAGTTGGTCCACAAAGAAAGGACCCCAACCAAGCCCAACCTCAG	712
OY	2586	GTTAAGCTGAGCGGATATACACACAGAGAAAAAGAGTTCTGGAAGCAGGCATGGGAAAAGT	2645
Db	713	GTTAAGCTGAGCGGATATACACACAGAGAAAAAGAGTTCTGGAAGCAGGCATGGGAAAAGT	771
OY	2646	CACCTCGGCATATTTGGGGAGAGAGCCCTCCAGGCCAGACTAATCTCAGAGACAGCTGT	2705
Db	772	CACCTCGGCATATTTGGGGAGAGAGCTCACTCCAGGCCAGATTAATCTCAGAGACAGCTGT	831
OY	2706	GGTGGCCCTCACTCAGAGACAGCCCTCCAGAGGACAGCCAGAGGGAGCCACTCTGGCCCTCA	2765
Db	832	GGTGGCCCTCACTCAGAGACAGCCCTCCAGAGGACAGCCAGAGGGAGCCACTCTGGCCCTCA	883
OY	2766	GACCAATTTCTGAGGCGACGCATTTGGGGGAGCCATGCTGGGCCAGACACCTTCAGAGAGGC	2825
Db	884	-----CTGGGCCCAAAACCACTTCAGAGAGGC	909
OY	2826	TGTCCGGGGAGGCACCTCCGGACACAGACCCCTCAGAGGAGACTGTGGAGAGAGCCATTTCT	2885
Db	910	TGTCCGGGGAGGCACCTCCGGACACAGACCCCTCAGAGGAGACTGTGGAGAGAGCCATTTCT	969
OY	2886	GGACCAAGACACCTCAGAGGATGCTGTTGGGGGAGCCACGCTGGGCCAGATACCTCAGA	2945
Db	970	GGACCAAGACACCTCAGAGGATGCTGTTGGGGGAGCCACGCTGGGCCAGATACCTCAGA	1029
OY	2946	GGAGGCTGTAGGAGGAGGTACACGTGGCCCAACCATCTCGGAGGACAGCCATGAGGGAGC	3005
Db	1030	GGAGGCTGTAGGAGGAGGTACACGTGGCCCAACCATCTCGGAGGACAGCCATGAGGGAGC	1089
OY	3006	CACACTGACACAGACTACGTACGACGAGAGAGGCTCCAGGGGGACACGAGTGTATCCAAATCC	3065
Db	1090	CACACTGACACAGACTACGTACGAGAGAGGCTCCAGGGGGACACGAGTGTATCCAAATCC	1149
OY	3066	TCTAGCCCTGAGGACAGACACAGACCCCCCACTCACCTGTGCAGGGAACTACAC	3125
Db	1150	TCTAGCCCTGAGGACAGACACAGACCCCCCACTCACCTGTGCAGGGAACTACAC	1209
OY	3126	CCAGATATCTCCAGTACACTGATTTGGAGTCTCAGGACCTGTGAGGTATAGGACGCGATC	3185
Db	1210	CCAGATATCTCCAGTACACTGATTTGGAGTCTCAGGACCTGTGAGGTATAGGACGCGATC	1269
OY	3186	TCAGGGGGCCTCAGAAATCTCAGG - CCCAGGAGAGGAACTACTAGGAGGAGAGCTG	3244
Db	1270	TCAGGGGGCCTCAGAAATCTCAGGAGCCCCAGAGAGGAGAACTACTAGGAGGAGAGCTG	1329
OY	3245	GAGGTCAAGGAATAGGCTGATTCGATGCGTATGCGAGGGATCTAAGGGCCTTACTGATCAGG	3304
Db	1330	GAGGTCAAGGAATAGGCTGATTCGATGCGTATGCGAGGGATCTAAGGGCCTTACTGATCAGG	1389
OY	3305	CCATATTTTATGCTGTACACACACTGCCCTGGTATGCCCATTTTGGTGGAGCTATGGCCCA	3364
Db	1390	CCATATTTTATGCTGTACACACACTGCCCTGGTATGCCCATTTTGGTGGAGCTATGGCCCA	1449
OY	3365	TACCTGCAGAGGCTTAGAGCTGACCCACCTGTGTGGGAGCTGTGAAACAATCCAGAGAGA	3424
Db	1450	TACCTGCAGAGGCTTAGAGCTGACCCACCTGTGTGGGAGCTGTGAAACAATCCAGAGAGA	1509
OY	3425	ATTGGGTGTCTCTCTTCTATCAGAGTACGTTGGTGTATGATCAATAGGACATATG	3484
Db	1510	ATTGGGTGTCTCTCTTCTATCAGAGTACGTTGGTGTATGATCAATAGGACATATG	1569
OY	3485	TCCAAACCAATGGAAATTTGGAACACCCGCTGGTCTCAGACTACAGACTGTACGCT	3544

Db	1570	TCACACCATATGGAAATTTGGACACCCGGCTGCTCAGCTACATGCACCTGCACGCT	16299
Qy	3545	GGGTACTACTAGTCAGGCGCTATGTCCACACACAGGCTCTCTAGATGTGAAGAACATCG	3604
Db	1630	GGGTACTACTAGTCAGGCGCTATGTCCACACACAGGCTCTCTAGATGTGAAGAACATCG	16899
Qy	3605	CCACACGACAAAGTTTGGGGAGATATCCCCACACCACTAA	3648
Db	1690	CCACACGACAAAGTTTGGGGAGATATCCCCACACCACTAA	1733
RESULT 6			
AAH06343			
ID	AAH06343	standard; CDNA; 638 bp.	
XX	AAH06343;		
XX	26-JUN-2001	(first entry)	
DT	26-JUN-2001	(first entry)	
DE	Human CDNA clone (5'-primer) SEQ ID NO:3178.		
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
PN	EP1074617-A2.		
PD	07-FEB-2001.		
XX	28-JUL-2000; 2000EP-0116126.		
PF	28-JUL-2000; 2000EP-0116126.		
XX	29-JUL-1999; 99JP-0248036.		
PR	27-AUG-1999; 99JP-0300253.		
PR	11-JAN-2000; 2000JP-0118776.		
PR	02-MAY-2000; 2000JP-0183767.		
XX	09-JUN-2000; 2000JP-0241899.		
PA	(HELI-) HELIX RES INST.		
XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX	WPI: 2001-318749/34.		
XX	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length CDNA defined in the specification, and for the detection		
PT	and/or diagnosis of the abnormality of the proteins encoded by the		
PT	full-length CDNA -		
PS	Claim 1; SEQ ID 3178; 2537bp + CD ROM; English.		
XX	The present invention describes primer sets for synthesizing 5602		
CC	full-length CDNA defined in the specification. Where a primer set		
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary		
CC	to the complementary strand of a polynucleotide which comprises one of		
CC	the 5602 nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	sequence and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in		
CC	the specification. The primer sets can be used in antisense therapy and		
CC	in gene therapy. The primers are useful for synthesizing polynucleotides,		
CC	particularly full-length CDNA. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		
CC	the full-length CDNA. The primers allow obtaining of the full-length		
CC	CDNA easily without any specialised methods. AAH03166 to AAH13628 and		
CC	AAH13633 to AAH18742 represent human CDNA sequences; AAH92446 to		
CC	AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632		
CC	represent oligonucleotides, all of which are used in the exemplification		
CC	of the present invention.		


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QY 1296 GCGCTTGGGAGGTTCTTGTGAGATCAACTGAGACCGTGGAGAGGACAACATGAGGA 1355
DB 2465 CCGACCCCACTGGCCGATGTCTCAGAGTCCAGACAGCTTACGATTTGGTGAATTCGAGGA 2524
QY 1356 GGACATATGAGAGAG-----ACGGAGGAGGAGAGAC 1387
DB 2525 TCGGATTAAGAGAGAGATCTCAGACAGGTACTGGCCATTGGATTGGTGGACACCGCC 2584
QY 1388 CCGGAGAGCCCGCTGTCTCCCAATCTGACATGCG----- 1423
DB 2585 TATGATGTGTATACCTACGCGGATACGGCCATTCGCGTCCCGCGGAAAAGCTGACAG 2644
QY 1424 -----CAGTCTACAGTCTCG 1439
DB 2645 CAATGCCCTGTCTGACAGTCTGCGCGGAGAGAGAGATGCGTGTGCTCCGTCTTAA 2704
QY 1440 CACAGGGGCTGGTCTGACCAAAATATGATGATACATGCACTGTGGACACGACCA 1499
DB 2705 GGTGTATTATGCTGACGATGCCCAATGCTTGTGACATGCAATTCATGATACGGGGA 2764
QY 1500 CCTGAGGTACCCAGCCGATCTTGGGATCATGTGCGCTGGAGAGCTGGGCTTGC 1559
DB 2765 TCCGGAGAGCGCGTGGCCGATCCAGACATCCACAAGATGACGAGACTAGGTTGCT 2824
QY 1560 CGGGCGCTGCTCACTGACACCGCGCTGCGACAGAGGCTGAGCTGCTCAGCTGCA 1619
DB 2825 GAACAGATGAAGCAACTGTCCCGGAGGCGGACACAGACGAGTGTGCTGCGCCA 2884
QY 1620 CAGTGTCTAGTACGTGGGTCTATCTCCGGGCGACAGAAATGAAAACCGGGAGCTGA 1679
DB 2885 CACTGCGCGCCATGTAATACAGTGTGCTGCGGCGCGAGCCGACAGAACTGCA 2944
QY 1680 CCGTGTGAGATTCACAACTTGAATCCATATATGCCCCAGTACTTGGCTGGCTGCA 1739
DB 2945 TGAGGCTGTGGATCTACAACTGCGGTATGTGATCGCCACCTTGTGATGGCCAC 3004
QY 1740 GCTTGCACACTGGCGCTGCGCTGCGGAGGTGAGGCTGTCTCAGAGAGAGTCTGAA 1799
DB 3005 CCGTGGCGCGCGTGTAGTGTGACAGGCGGTGAGAGTGTGCTGGGAGATCCCGGAG 3064
QY 1800 TGTGTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1859
DB 3065 CGGCTGTGCAAGCTGCTGCGCGCGGCGGATCATCCAGAGATTCCTCCAGCGCTT 3124
QY 1860 TTGCTTTTCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1919
DB 3125 CTGATTTTCAACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3183
QY 1920 CTTAGGATCTGATTTGTGATTTGGATGTCACACGAGTATAGAGTACAGCATGTT 1979
DB 3184 --AGCGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3241
QY 1980 TGAGGATGACCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2039
DB 3242 CGAATCCCAATCCCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3301
QY 2040 CCGCATGGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2099
DB 3302 CCGCAAGGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3361
QY 2100 CCGTACAGGTGATGAGAGGCGCGCGGATGAGTGTGTGTGTGTGTGTGTGTGTGT 2159
DB 3362 TGTGACATATACCTGAGAGAGAGGATGAGTGTGTGTGTGTGTGTGTGTGTGTGT 3421
QY 2160 TCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2219
DB 3422 GCACGTATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3481
QY 2220 CTTTGTATGCTGACAGGCGGATGCGGTGGGGGCTGCCAGGTACCTGAGAGGTTATGC 2279
DB 3482 ATTGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3541
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QY 2280 CCACTTCACCCACTGCTGTATGAGGCTTGGCCAGTGGCCGATTTATCCTTACAGAGG 2339
DB 3542 CATGCTACACCCACTGCTGTGCTGTGGCCAGCGCGGATTAATGCTTTCGGAAGG 3601
QY 2340 TGGCTATTAACCTGATACATCCATCTCAGAGTGCATGAGTGCCTGCTGCTGCTGCT 2399
DB 3602 TGGCTACAAATGTAATCTCATTTCTGACGAGATGACCATGATGACCAAGAGCTGTGG 3661
QY 2400 AGACCC 2405
DB 3662 TGTATCC 3667

RESULT 9
AAV87399
ID AAV87399 standard; cDNA; 424 BP.
AC AAV87399;
XX
XX
XX 27-APR-1999 (first entry)
DE EST clone CD146.
XX
XX
XX Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; actinin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
XX Homo sapiens.
OS
XX WO9845435-A2.
PN
XX 15-OCT-1998.
PD
XX 10-APR-1998; 98WO-US06954.
XX
XX 10-APR-1997; 97US-0835913.
XX
XX (GENE ) GENETICS INST INC.
XX
XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
XX WPI; 1999-070076/06.
XX
XX
XX New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries
XX
XX Claim 1; Page 551; 633pp; English.
XX
XX This sequence represents an expressed sequence tag (EST), and is a
CC polynucleotide of the invention. The polynucleotides of the invention are
CC all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC actinin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene
CC therapy.
XX
XX Sequence 424 BP; 89 A; 140 C; 109 G; 86 T; 0 other;
SQ
Query Match 10.9%; Score 398.4; DB 20; Length 424;
Best Local Similarity 98.5%; Pred. No.2.3e-96;
Matches 402; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2178 TGCTTACAGATTAAACCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2237
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Db      15 TGGCTAGAGTTTAAACCAAGACTGCTGCTGCTACACTGAGCTTGTATGCTGCACGGGG 74
Oy      2238 GGATCGGCTGGGGGGGTCGCCAGGTGTACCTCGAGGGTATATGCCACCTCACCCTCT 2297
Db      75 GGATCCGCTGGGGGGGTCGCCAGGTGTACCTCGAGGGTATATGCCACCTCACCCTCT 134
Oy      2298 GATGGGCTTGGCCAGTGGCCGCTATATCTTATCTTAAGGGTGGCTATACCTGACATC 2357
Db      135 GATGGGCTTGGCCAGTGGCCGCTATATCTTATCTTAAGGGTGGCTATACCTGACATC 194
Oy      2358 CATCTCAGAGTCCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2417
Db      195 CATCTCAGAGTCCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
Oy      2418 GACCCCTCCCAAGGCCCCCATATATAGAGGGCCCTGGCTCAATCATCTAGACATCAAT 2477
Db      255 GACCCCTCCCAAGGCCCCCATATATAGAGGGCCCTGGCTCAATCATCTAGACATCAAT 314
Oy      2478 CCATCCGAGATATCTGGCGCAGCTTACGGGTCATGATAGAGTAGAAGAGAGACCCCTC 2537
Db      315 CCATCCGAGATATCTGGCGCAGCTTACGGGTCATGATAGAGTAGAAGAGAGAGACCCCTC 374
Oy      2538 CAGTTCTAAGTGTGTACCAAGAGGACACCCCAACGACCAACCTAG 2585
Db      375 CAGTTCTAAGTGTGTACCAAGAGGACACCCCAACGACCAACCTAG 422

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RESULT 10
AAC76966
ID AAC76966 standard; cDNA; 2461 BP.
AC AAC76966;
XX
XX
XX 08-FEB-2001 (first entry)
DE Human ORFX ORF2521 polynucleotide sequence SEQ ID NO:5041.
XX
XX
XX Human: open reading frame; ORFX; detection: cytostatic; hepatotropic;
KW vulnerable; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
KW anticonvulsant; osteopathic; antiallergic; immunosuppressant; cardiac;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antineoplastic;
KW antiviral; antibacterial; antifungal; antineoplastic; antihypertensive;
KW antineoplastic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antineoplastic disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
XX Homo sapiens.
XX
XX PN MO200058473-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000MO-US08621.
XX
XX 31-MAR-1999; 99US-0127607.
XX 02-APR-1999; 99US-0127636.
XX 05-APR-1999; 99US-0127728.
XX 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
XX
XX WPI; 2000-602362/57.
XX P-PSDB; AAB42757.
XX

PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 5; Page 4224-4225; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnerable;
XX antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
XX osteopathic; anticonvulsant; antiallergic; immunosuppressant;
XX immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
XX antidiabetic; hypotensive; dermatological; immunosuppressive;
XX antineoplastic; antibacterial; antiviral; antifungal; antineoplastic;
XX antihypertensive; and antineoplastic. The sequences can be used for determining
XX the presence of or predisposition to, or preventing or treating
XX pathological conditions associated with an ORFX-associated disorder. The
XX nucleic acids can be used to express ORFX proteins in gene therapy
XX vectors. The proteins and nucleic acids may be used to treat cancers,
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,
XX graft vs host disease, cardiovascular disease, diabetes mellitus,
XX hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
XX erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
XX bacterial or fungal infection, malaria, autoimmune disorders, asthma,
XX allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
XX nocturnal haemoglobinuria, antineoplastic disease; to enhance
XX coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 2461 BP; 409 A; 815 C; 815 G; 422 T; 0 other.

Query Match 9.5%; Score 347.6; DB 21; Length 2461;
Best Local Similarity 60.5%; Pred. No. 2.2e-82;
Matches 572; Conservative 0; Mismatches 374; Indels 0; Gaps 0;

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Oy      319 GAAGCCCTGAGCGGCTCCATGATCAAGAGAGCAACATGAGAGGCTCTAGAT 378
Db      376 GAGCGCTCTGAGCGGCTCCATGATCAAGAGAGCAACATGAGAGGCTCTAGAT 435
Oy      379 CGTCCGCTGCTCTTCAAGCGCCGCTTGTGCTGAAAAGAGAGCTGATGTTGCACAGC 438
Db      436 AGGTGCTGCGGCTGTCAGCCCGGAGGCTTCGGAAGAGAGCTGAGCTGCTGTCACAGC 495
Oy      439 CTAGATATATGATCTGATGAGAAACACCCAGTACATGATGAGAGGAGACTCCGTGTC 498
Db      496 CCAGATATGATCTGATGAGAGGAGGAGGAGGCTGATGAGAGAGGAGGAGGAGG 555
Oy      499 CTAGAGACACTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 558
Db      556 CTGTCGAGAGCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 615
Oy      559 GCGTCAGGCTGTCCTGAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 618
Db      616 GCGCAGAGGCTGTCCTGAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 675
Oy      619 ATGGCCATCATTAAGGCTCTGAGCATACGCCGCCAGCAGCTTATGATGCTATTTGC 678
Db      676 CTTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 735
Oy      679 ATGTTCAACACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 738
Db      736 GTGTTCAACACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 795
Oy      739 GTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 798
Db      796 ATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 855
Oy      799 GACCCAGTGCCTCTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 858
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Oy      859 CTGAAGGCTCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 918
Db      916 CTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 975

```


[illegible]

RESULT 12
AAD36979
ID AAD36979 standard; cDNA; 2022 BP

DT	21-AUG-2002	(first entry)
XX		
DE	Human histone deacetylase cDNA.	
XX		
KV	Human; histone deacetylase; therapy; cancer; bait protein; cytosolic	
KW	enzyme; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..2022
FT		/*tag= a
FT		/product= "Human histone deacetylase"

XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-EP11759.
XX
PR 13-OCT-2000; 2000US-239928P.
XX
PA (FARB) BAYER AG.
XX
PI Zhu Z;
XX

PT New human histone deacetylase polypeptide useful for identifying
PT modulating agents that can be used for treating diseases such as cancer
XX
XX
PS
PT
XX
XX
Claim 1; Fig 1; 116pp; English.
CC The present invention relates to novel histone deacetylase proteins and
CC polynucleotides encoding them. Sequences of the invention are useful for
CC identifying modulating agents that are used for preventing, ameliorating
CC treating or correcting dysfunctions or diseases such as cancer. They can
CC also be used to screen for human histone deacetylase activators and
CC inhibitors. They are useful for generating antibodies and can be used as
CC bait proteins in two-hybrid assay or three-hybrid assay. The present
CC sequence is a cDNA encoding human histone deacetylase.
XQ Sequence 2022 BP; 341 A; 642 C; 665 G; 374 T; 0 other;

[illegible]

QY 379 CGCTGCGTGCCTTTCAAGCCCGGTTTCTGTAAGAAAGAGAGCTGATGTGGTTGCACAGC 438
 Db 136 AGGTGTCTGCGGTTGTCAAGCCCGGAGCGCTTCGGAAGAGAGAGCTGGCGCTGGTGCACAGC 195
 QY 439 CTAGAAATTTATTTGATCTGATGGAAGAAACCAACCAGTACATGATGAGGGAGAAATCCGTGTC 498
 Db 136 CCAGAGTATGATCCCTGGTCAAGGAGAGACCAGGTCCTTAGGCCAAGAGAGAGCTGCAGCGC 255
 QY 499 CTAGAGACACCTTACAGCTCAGTTTATCTGATCCGGAATCTACATATCTCTGGCCCTCGTG 558
 Db 256 CTGTCCGACAGATTGACAGCCCATCTACTTCCACCCGATACCTTTCACTGCGCGCGCTG 315
 QY 559 GCGTCAGGCTCTGTCTCCAGGCTGGTGGATCGGCTCTGGGGGCGTGAGATCCGGAATGAC 618
 Db 316 GCGCGAGGGGCTGGGACCTGACAGCTGGTGGAGCGTGTGCTACATGGAGCTGTGCAGAAATGG 375
 QY 619 ATGGCCATCATTAGGCTCTCTGAGCATACGCCCAAGCACAGTCTTATGATGGCTATTGC 678
 Db 376 CTGGCCCTGGTGAAGGCTCCCGGGGACCATGGCCAGAGAGGGGCGTCCACAGGGGTTTCTGT 435
 QY 679 ATGTTCAACACAGTGGGCTGTGGGACCGCGGTATGCTCAAGAAACACCGCATCCGGAGG 738
 Db 436 GTGTTCAACAACGTGGCCATATGACAGCTGACATGCTCAACAGCAAGAAACAGGGCTTACACAGG 495
 QY 739 GTCCATTATCTAGATTGGAGTGTGACACACGGTCAGAGAACACATTCCTTGACACAG 798
 Db 496 ATCCCTCGTGTGAGACTGGGATGTGACCATGGCCAGGAGATCCAGTAATCTCTTTGAGGAT 555
 QY 799 GAACCCAGTGTCTCTATTCTTCTCATCCACCGCTACGACAGGGTAGTCTTGCGCCAC 858
 Db 556 GACCCAGACGCTCTTACTTCTCCGTGGACACCGCTATGAGCATGTGGCGCTTCTGGGCTTTC 615
 QY 859 CTGAAGGCGCTTAACTGTGTCACACCAAGAGTTTCGGGCCAAGGCCAAAGATATACCATCAAT 918
 Db 616 CTGGAGAGGTAGATGACAGACGACAGTGGGGGCGGGGACAGGGCTTCGGCTTCACTGTCAAC 675
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 Db 676 CTGCGCTTGAAACAGAGTTGGGATGGAAGAAAGCTTACATCTGTCGTGCGCTTCTGTGACCTG 735
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 QY 1099 ACCCAACCGTCATAGGCTGTGGACAGAGGACAAGCTGATCTGTCTGTGAGAGGTGGCTAC 1158
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 QY 1159 AACCTCGCGCGCTGGCTGAAGAGCGTCAAGTCTTCTGCTCCACACCTTCTTGGAGACCTT 1218
 Db 916 CACCTGAGTCACTGGCGGAGTCAAGTGTGATGACAGTACAGACGATGCTGGGTGACCCG 975
 QY 1219 TGCCCCATGCTGAGAGTCACTGTGTGTGCCCTTCCGCGGAGTGGCCAGG 1264
 Db 976 GCCCCACCCCTGTCAAGGGCCAAATGGCGCATGTCAAGAGTGTCCAGG 1021

XX	RESULT 13
XX	ABQ73030
ID	ABQ73030 standard; cDNA; 2104 BP.
XX	
AC	ABQ73030;
XX	
DT	23-SEP-2002 (first entry)
XX	
DE	Human HDAC9 variant HDAC9v2 encoding cDNA sequence SRO_ID NO:7.
XX	
XX	Human HDAC9; histone deacetylase related gene; histone deacetylase
KW	cytosolic; antiproliferic; antithrombotic; antiinflammatory;

PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225757.
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PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 08-SEP-2000; 2000US-0231242.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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PR 14-SEP-2000; 2000US-0232399.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0233423.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251988.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465566/50.
P-PSDB; AAU23410.

Novel polypeptides and polynucleotides useful for diagnosing,
preventing, treating neural, immune system, muscular, reproductive,
pulmonary, cardiovascular, renal, proliferative disorders and cancerous
diseases

XX Claim 4: SEQ ID No 506; 1180bp; English.
 PS The present invention relates to the isolation of novel human enzyme
 CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders, including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
 CC blood-related disorders (e.g. haemophilia), reproductive disorders
 CC (e.g. infertility) and infectious disorders (e.g. Influenza). The
 CC polynucleotides of the invention can also be used in gene therapy.
 CC AAS40785-AAS41684 represent cDNA sequences encoding for the novel human
 CC enzyme polypeptides of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 XX

Sequence 1005 BP; 167 A; 313 C; 332 G; 183 T; 10 other;

Query Match 8.9%; Score 325.8; DB 22; Length 1005;

Best Local Similarity 60.7%; Pred. No. 9.8e-77;

Matches 522; Conservative 4; Mismatches 334; Indels 0; Gaps 0;

319 GAAGGCCCTGAGCGGCTCCATCATCAAGAGCACTGATCCAGAGGCGCTCTAGAT 378
 118 GAGCGCTGAGCGGCTCCATCATCAAGAGCACTGATCCAGAGGCGCTCTAGAT 177
 379 CGCTGCGTCTCTTTCAGGCGCGGTTGCTGAAAGAGAGCTGATGTTGTTCAAGC 438
 178 AGGTGCTGCGGTTGCTGAGCGCGGCTGCGAGAGAGAGCTGAGGCTGCTGACAGC 237
 439 CTAGATATATGATGATGATGAGAAACACCACTATGATGATGAGAGAGAGCTGCTG 498
 238 CAGAGTATGATGATGATGATGAGAAACACCACTATGATGATGAGAGAGAGCTGCTG 297
 499 CTAG 558
 298 CTGTCGGAG 357
 559 GCGTCAGGCTGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 618
 358 GCGGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 417
 619 ATGGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 678
 418 CTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
 679 ATGTTCAACACAG 738
 478 GTGTTCAACACAG 537
 739 GTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 798
 538 ATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597
 799 GACCCAG 858
 598 GACCCAG 657
 859 CTGAAGGCTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 918
 658 CTGAG 717
 919 GTGCTTGAAG 978
 718 CTGCTGAG 777

QY 979 CTGCTGAG 1038
 DB 778 CTGCTGAG 837
 QY 1039 GCGCTGAG 1098
 DB 838 TCAAG 897
 QY 1099 ACCAG 1158
 DB 898 ACAG 957
 QY 1159 AACCTGAG 1178
 DB 958 CACCTGAG 977

Search completed: June 13, 2003, 19:39:13
 Job time : 762 secs

QY	2128	ATGGGTGATGCTGACTACTACCTACCTAGCTGCGGCATGCGCTGGTGGCTTCCCATTTGGCTACAG	2187
Db	2231	ATTGAGAGCGTGGAGTACCTTACCAAGCCTTCAGAGACAGTGTGTGATGCCATTGGCCACAGC	2290
QY	2188	TTTAAACCCAGACTGGTGTGCTGTCTACAGCTGCGCTTTGATGCT----	2241
Db	2291	TTTCACACTCTGATGTGGTCTCAGTGTCCCGCGGGTTTGTATGCTGTGAAGGACATCTGTCT	2350
QY	2242	CCGCTGGGGGGCTGCGACAGTGTCAACCTGAGGGTTATGTGCCACACCTACACCTGCTGATG	2301
Db	2351	CCTGTGGGTGGCTTACTGTGTCAACGCCAGATGTTTGGCCACTTGACCAAGCAGCTGATG	2410
QY	2302	GGCCTTGGCAATGGCGCATTAATCCTTATCTAGAGGGTGGCTATTAACCTGACATCATC	2361
Db	2411	ACCTGTGCGAGGGGGCCGGGTGTGTGTGCGCTGTGAGGAGGCCATGACTTGACCGCATC	2470
QY	2362	TCAGAGTCCATGGTCTGCTG	2381
Db	2471	TGTGATGCTCTGAAGCTTG	2490

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1      RESULT 2
2      US-08-216-894-1
3      ; Sequence 1, Application US/08216894
4      ; Patent No. 5876734
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Kirchoff, Louis V.
7      ; APPLICANT: Otsu, Keiko
8      ; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
9      ; TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
10     ; NUMBER OF SEQUENCES: 10
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: Foley & Lardner
13     ; STREET: 3000 K Street, N.W., Suite 500
14     ; CITY: Washington, D.C.
15     ; COUNTRY: USA
16     ; ZIP: 20007-5109
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: Floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/216,894
24     ; FILING DATE: 24-MAR-1994
25     ; ATTORNEY/AGENT INFORMATION:
26     ; NAME: BENT, Stephen A.
27     ; REGISTRATION NUMBER: 29,766
28     ; REFERENCE/DOCKET NUMBER: 85326/102/DR10
29     ; TELECOMMUNICATION INFORMATION:
30     ; TELEPHONE: (202)672-5300
31     ; TELEFAX: (202)672-5399
32     ; TELEX: 904136
33     ; INFORMATION FOR SEQ ID NO: 1:
34     ; SEQUENCE CHARACTERISTICS:
35     ; LENGTH: 1695 base pairs
36     ; TYPE: nucleic acid
37     ; STRANDEDNESS: double
38     ; TOPOLOGY: linear
39     ; MOLECULE TYPE: DNA (genomic)
40     ; FEATURE:
41     ; NAME/KEY: CDS
42     ; LOCATION: 1..1692
43     ; US-08-216-894-1

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	Best Local Similarity	44.0%	Pred. NO. 0.00027;		
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QY	2618	AGGTTCTGGGAAGCAGGCATGGGGAAAGTACACTCGGCATCATTTTGGGGAAAGATCCACTC	2677
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Dd	1340	AAGCCACAGAAAGTTGCCGGAAGCCGAGAAAGCAGAAAGCAGCTGAAGCCACGAAAGTTGCCG	1399
QY	2798	TGCTGGGCCAGACCACTCCAGAGAGAGGCTGTCCGGGGAGCCACTCCGAGCCAGACCACT	2857
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RESULT 3
 US-09-115-746-1
 ; Sequence 1, Application US/09115746
 ; Patent No. 6228601
 ; GENERAL INFORMATION:
 ; APPLICANT: Kirchhoff, Louis V.
 ; APPLICANT: Otsu, Keiko
 ; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
 ; TITLE OF INVENTION: WITH TRIPANOSOMA CRUZI
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/115,746
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/216,894
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1695 base pairs
 ; TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1692
 US-09-115-746-1

Query Match 1.4%; Score 51.4; DB 4; Length 1695;
 Best Local Similarity 44.0%; Pred. No. 0.00027;
 Matches 217; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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 1220 CGAAGGTTGCCGAGAGCGGAGAACAGAGGCGAGCTGAAGCCATGAAGTTGCCGAGCGG 1279
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 1280 AGAAGCAGAGGAGCTGAGGCGACGAAAGGTTGCCGAAAGCGAGAGACAGAGGAGCTG 1339
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 1520 TTGCCGAGAGCGAGAGAGAGGCGAGCTGAGAGGCTGTGCCGAGAGCGAGAGG 1579
 2978 CCATCTCGGAGAGGAGCGATGAGGAGCGACACTGAGACGACTAGCTCAGAGAGGCTC 3037
 1580 AGAAGCAGCTGAAGCGAGAGGTTGCCGAAAGCGAGAGAGAGAGGAGCTGAAGCCA 1639
 3038 CAGGGGCGACCGA 3050
 1640 CGAAGGTTGCCG 1652

RESULT 4
 US-08-216-894-7
 Sequence 7, Application US/08216894
 Patent No. 5876734
 GENERAL INFORMATION:
 APPLICANT: Kitchoff, Louis V.
 APPLICANT: Otsu, Keiko
 TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
 TITLE OF INVENTION: WITH TRYPAOSOMA CRUZI
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/216,894
 FILING DATE: 24-MAR-1994

ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 85326/102/DRLO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1932 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1929
 US-08-216-894-7

Query Match 1.4%; Score 51.4; DB 2; Length 1932;
 Best Local Similarity 44.0%; Pred. No. 0.00029;
 Matches 217; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

2558 AGAAGCACCACCCACCAACCTAGTGTAGCTGAGCGATGACACAGAGAAAGA 2617
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 1160 AGAAGCAGCTGAGCGCCGCAAGGCGCTGAGAGCGAAGAGAGGCGAGCTGAAGCCA 1219
 2618 AGGTTCTGGAAGCAGGCGATGGGAAAGTCACTCGCATCATTTGGGAAAGTCCACTC 2677
 1220 CGAAGGTTGCCGAGAGCGGAGAACAGAGGCGAGCTGAAGCCATGAAGTTGCCGAGCGG 1279
 2678 CAGCCAGACTAACTAGAGACAGCTGTGTGCTCTCACTCAGGACCGCTCAGAGG 2737
 1280 AGAAGCAGAGGAGCTGAGGCGACGAAAGTGTGCCGAAAGCGAGAGAGGAGCTG 1339
 2738 CAGCCACAGGGGAGGCGACTGTGGCCAGACCATTTTGAAGGAGCGCATTTGGGGAGCCA 2797
 1340 AAGCCACAGAGGAGGTTGCCGAAAGCGAGAGAGAGGCGAGCTGAAGCCAGAGGTTGCCG 1399
 2798 TGCTGGGCGCAGACACCTCAGAGAGGCTGTGGGGGAGGCGACCTCGGACCGAGACCT 2857
 1400 AAGCGAGAGAGAGAGGCGAGCTGAGAGCGACGAAAGTTGCCGAAAGCGAGAGAGG 1459
 2858 CAGAGAGACTGTGGGAGAGGCGATTTCTGACCGACGACCTCAGAGAGTGTGGGG 2917
 1460 CAGCTGAAGCGCAGAGGTTGCCGAAAGCGGAGAGACAGAGGAGCTGAAGCCAGAGAGG 1519
 2918 GAGCCAGCTGGGCGAGACTTCACTCAGAGAGGCTGTGAAGAGAGCTTACCTGGCCAGA 2977
 1520 TTGCCGAGAGCGAGAGAGAGGCGAGCTGAAGCGACGAGGTTGCCGAAAGCGGAGAGG 1579
 2978 CCATCTCGGAGAGGAGCGATGAGGAGGCGACACTGAGACGACTAGCTGAAGAGAGGCTC 3037
 1580 AGAAGCAGCTGAAGCGAGAGGTTGCCGAAAGCGAGAGAGAGAGGAGCTGAAGCCA 1639
 3038 CAGGGGCGACCGA 3050
 1640 CGAAGGTTGCCG 1652

RESULT 5
 US-09-115-746-7
 Sequence 7, Application US/09115746
 Patent No. 6228601
 GENERAL INFORMATION:
 APPLICANT: Kitchoff, Louis V.
 APPLICANT: Otsu, Keiko
 TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
 TITLE OF INVENTION: WITH TRYPAOSOMA CRUZI
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner

Db	3942814	CAGAGGGGGCAGTGTGTGGCGCGCGCGAGAGGTATCGTGTGGCGCTCGCGCGGCGCAAGG	39428173
Oy	2753	CCACTCTGCGCCACACCATTTCTGAGCGAGCCATTGGGGGAGGCGCATGTGCGGCCAGACCA	2812
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Oy 2993 CCATGGAGGAGCCACACTGACCCTACGTACGTACAGAGGAGCCTCCAAGGGGCACCGAG 3051
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Db 3936661 CGGCGGGCGGCCGCCGACCGAGGCGCACGGGCGCGCCGCCGGCGGCACACCGAAG 3936719

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RESULT 11
US-08-342-930-1
; Sequence 1, Application US/08342930
; Patent No. 5821084
; GENERAL INFORMATION:
; APPLICANT: OLMSTED, ELIZABETH A.
; APPLICANT: MAURO, LAURA J.
; APPLICANT: DAVIS, ALAN R.
; APPLICANT: DIXON, JACK E.
; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,930
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20975.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 205..5337
; US-08-342-930-1

Query Match
Best Local Similarity 1.1%; Score 40.4; DB 1; Length 5455;
Matches 101; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 3320 TGACGACACTGCGCTGGTGTCCTCCATTTGGTGGCAGTATGCCCATCTGACAGCAGGCC 3379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2230 TGGGCCCAAGTCTCGGGGGCCGAGCCGCTACCAAGTAGCCCTATACGAGAGATACC 2289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3380 TAGACTGACCCCACTGTGGGGAGCTGTGGAACAATCCAGAGAAATTGGGTGTCTCT 3439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2290 CGGACGACCAACGCAATCATGAGGGGCCCAAGAGATGGCACGAGCTTTGGGTTTACT 2349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3440 CTTCGATCAGAGCTGTGTGTCGTTTACATCATGCGACATGCTCCACACACAGTGA 3499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2350 CCTGGACATCAAGTCAAGTGAAGTCAATCTCTCTGGGCTGGGCCCTTACACTGCAGCA 2409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3500 ATTCTGACACCGCGTGTGCTCT 3521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2410 GCCAAGCTTCTGCTGAGACT 2431
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RESULT 12
US-08-983-045-1/c
; Sequence 1, Application US/08983045
; Patent No. 6093535
; GENERAL INFORMATION:
```

```
APPLICANT: MORI, Chisato
APPLICANT: TAKAHARA, Rie
APPLICANT: OSAME, Juichiro
APPLICANT: GOMI, Yasuyuki
APPLICANT: FUKE, Isao
; TITLE OF INVENTION: METHOD FOR IDENTIFYING THE ATTENUATED VARICELLA VIRUS OKA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,045
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP97/01646
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-158795
; FILING DATE: 15-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 216-393P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: varicella-zoster virus
; STRAIN: attenuated varicella virus Oka strain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..486
; US-08-983-045-1

Query Match
Best Local Similarity 1.1%; Score 40.2; DB 3; Length 487;
Matches 129; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 350 GCGGCCGAGTGGGCGGACGCGGAGATTCGGGAAGCGGCGAGGTGGGCGG 291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2797 ATGCTGGGCCAGACCACTCTAGAGAGAGCTGTGGGGGAGGCACATCCCGGACAGACACC 2856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 290 ACGGCGGGATCGGATTTTGGGGAAGCGGCCAGAGTGGGCGGACGCGGGATTCGGGATT 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2857 TCAGAGGAGACTGTGGAGAGACCATTTTGAGACAGACCACTCAGAGAGTCTGTTGG 2916
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 230 CGGGTAGCGGCCAGAGTGTGGCGCGAGCGGGGATGTGGCTTTCCGGGAAGCGGCCAGAGTG 171
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QY 2917 GGAGCCAGCTGGGCCAGACTACTCTAGAGAGAGCTGTAGAGAGAGCTTACACTGGCCAG 2976
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DB 170 GCGCGAGAGCGGGATCGGGCTTTCGGGAAGCGGCCGAGTGGGCGGACGCGGGAGTCG 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2977 ACATCTCGAGGAGGAGCATGTGAGAGGAGCCACACTGG 3013
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Db 110 GGCCTTCGGGAAGCGCCGAGGTGGGCGGACGGCGG 74

RESULT 13

US-08-983-045-3/c

; Sequence 3, Application US/08983045
; Patent No. 6093535

GENERAL INFORMATION:

APPLICANT: MORI, Chisato
APPLICANT: TAKAHARA, Rie
APPLICANT: OSAME, Junichiro
APPLICANT: GOMI, Yasuyuki
APPLICANT: FUKE, Isao

TITLE OF INVENTION: METHOD FOR IDENTIFYING THE ATTENUATED VARICELLA VIRUS OKA STR

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,045

FILING DATE: 15-JAN-1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP97/01646

FILING DATE: 15-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-158795

FILING DATE: 15-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, Leonard R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 216-393P(PCT)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1683 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: varicella-zoster virus

STRAIN: attenuated varicella virus Oka strain

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1683

US-08-983-045-3

Query Match

Best Local Similarity 1.1%; Score 40.2; DB 3; Length 1683;

Matches 129; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Db 2737 GCAGCCACAGGGGAGGACCTCTGGCCACACCATTTCTGAGGACGACCATTTGGGGAGCC 2796

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Db 2797 ATGCTGGGCGGACGACCTCAGAGAGGCTGTGGGGGACCACTCCGAGCAGACACC 2856

Db 341 ACGGGGAGTTCGGATTCGGGAACGCGCGGAGGTGGGCGGACGCGGAGTTCGGATTC 282

Db 2857 TCAGAGGAGACTGTGGGAGGAGCCATTCTGAGCAGACCACTCAGAGGATGCTGTGGG 2916

Db 281 CGGATAGCGCGCCAGAGTGGGCGGACGCGGAGTCGGCTTTTCGGAAGAGCGCGGAGGTG 222

RESULT 14

US-09-446-504-79

; Sequence 79, Application US/09446504
; Patent No. 6218150

GENERAL INFORMATION:

APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshimi
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MUKAI, Hiroyuki

TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS

FILE REFERENCE: 1422-408PCT

CURRENT APPLICATION NUMBER: US/09/446,504

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: PCT/JP98/02845

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: JP 9-187496

PRIOR FILING DATE: 1997-06-26

PRIOR APPLICATION NUMBER: JP 9-320692

PRIOR FILING DATE: 1997-11-27

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 79

LENGTH: 1005

TYPE: DNA

ORGANISM: Pyrococcus furiosus

US-09-446-504-79

Query Match

Best Local Similarity 1.1%; Score 39.2; DB 4; Length 1005;

Matches 68; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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Db 658 GGGGATGGGATATACATATATGTTGGAGCAATGCTGCCAATAGTTGAAGAATT 717

Db 2191 AACCCAGACTGGTCTGCTCAGCTGCTGCTTGTGATCTGCACGGGGGATCCCT 2246

Db 718 AACCCAAAGTCAATCGAATTCGCGGCTTGTGATGATTAAGGGGATGCT 773

RESULT 15

US-09-712-266-79

; Sequence 79, Application US/09712266

; Patent No. 633158

GENERAL INFORMATION:

APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshimi
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MUKAI, Hiroyuki

APPLICANT: ASADA, Kiyozo

APPLICANT: KATO, Ikunoshin

TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS

FILE REFERENCE: 1422-408PCT

CURRENT APPLICATION NUMBER: US/09/712,266

PRIOR FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: US 09/446,504

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: PCT/JP98/02845

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Pyrococcus furiosus
US-09-712-266-79

Query Match 1.18; Score 39.2; DB 4; Length 1005;
Best Local Similarity 58.6%; Pred. No. 0.5;
Matches 68; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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DB 658 GGGATGGGATACATATATGTGTTGGAGAAATGTGCTTCCCATATAGTTGAAGAGTT 717
QY 2191 AACCCAGAACTGGTGGCTGCTCAGCTGGCTTGTATGTCACAGGGGGGATCGCT 2246
DB 718 AAGCCAAAGTCACTCTAATTTCGCGGCTTGATGATTTAAAGGGATGCTCT 773

Search completed: June 13, 2003, 16:41:18
Job time : 213 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 16:35:13 ; Search time 484 Seconds

(Without alignments)
10914.309 Million cell updates/sec

Title: US-09-800-187-5

Perfect score: 3648

Sequence: 1 atgacctcaacgcgcagca.....atagcccccacacacactaa 3648

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3614.4	99.1	4099	10 US-09-817-913-12	Sequence 12, Appl
2	3614.4	99.1	4099	10 US-09-817-538-12	Sequence 12, Appl
3	346	9.5	2022	10 US-09-976-280A-1	Sequence 1, Appl1
4	226.6	6.2	418	10 US-09-983-965-5409	Sequence 5409, Ap
5	210.6	5.8	3131	10 US-09-817-913-14	Sequence 14, Appl
6	210.6	5.8	3131	10 US-09-817-538-14	Sequence 14, Appl
7	194	5.3	8459	9 US-09-563-728A-31	Sequence 31, Appl
8	192.4	5.3	8459	10 US-09-817-913-8	Sequence 8, Appl1
9	192.4	5.3	8459	10 US-09-817-538-8	Sequence 8, Appl1
10	173.6	4.8	2233	9 US-09-563-728A-33	Sequence 33, Appl
11	173.6	4.8	2233	10 US-09-817-913-10	Sequence 10, Appl
12	173.6	4.8	2233	10 US-09-817-538-10	Sequence 10, Appl
13	153.2	4.3	3054	9 US-10-173-539-5	Sequence 5, Appl1
14	153.2	4.3	3186	9 US-10-072-094-97	Sequence 97, Appl1
15	155.2	4.3	3186	9 US-10-173-539-1	Sequence 1, Appl1
16	155.2	4.3	3650	9 US-10-072-094-94	Sequence 94, Appl
17	155.2	4.3	4467	9 US-10-072-094-88	Sequence 88, Appl
18	155.2	4.3	7689	9 US-10-173-539-14	Sequence 14, Appl
19	143.6	3.9	452	9 US-09-796-692-4129	Sequence 4129, Ap

20	143.6	3.9	452	9 US-10-040-862-4129	Sequence 4129, Ap
21	140.4	3.8	1452	10 US-09-822-830A-585	Sequence 585, App
22	139.4	3.8	343	10 US-09-783-590-10530	Sequence 10530, A
23	137.2	3.8	313	10 US-09-833-381-1303	Sequence 1303, Ap
24	133.2	3.7	451	9 US-09-796-692-3075	Sequence 3075, Ap
25	133.2	3.7	451	9 US-10-040-862-3075	Sequence 3075, Ap
26	127	3.5	141	10 US-09-783-590-3772	Sequence 3772, Ap
27	121.8	3.3	311	10 US-09-783-590-9596	Sequence 9596, Ap
28	121.8	3.3	559	9 US-09-918-995-28035	Sequence 28035, A
29	110.4	3.0	492	9 US-09-918-995-9706	Sequence 9706, Ap
30	106.2	2.9	3209	9 US-10-072-094-106	Sequence 106, App
31	105.8	2.9	489	9 US-10-072-094-12	Sequence 12, Appl
32	105.8	2.9	2790	9 US-10-072-094-98	Sequence 98, Appl
33	105.8	2.9	3367	9 US-10-173-539-7	Sequence 7, Appl1
34	105.8	2.9	3499	9 US-10-173-539-3	Sequence 3, Appl1
35	105.8	2.9	3550	9 US-10-173-539-13	Sequence 13, Appl
36	105.8	2.9	7303	9 US-10-173-539-15	Sequence 15, Appl
37	83	2.3	295	10 US-09-284-093B-1185	Sequence 1185, Ap
38	75	2.1	402	9 US-09-918-995-36187	Sequence 36187, A
39	67.8	1.9	299	10 US-09-294-093B-2333	Sequence 2333, Ap
40	59.2	1.6	340	9 US-10-072-094-17	Sequence 17, Appl
41	59.2	1.6	525	9 US-10-072-094-19	Sequence 19, Appl
42	59	1.6	122186	9 US-09-563-728A-36	Sequence 36, Appl
43	56.2	1.5	6072	9 US-09-764-881-8523	Sequence 8523, Ap
44	54.6	1.5	529	9 US-10-072-094-14	Sequence 14, Appl
45	54.6	1.5	1035	10 US-09-815-242-4004	Sequence 4004, Ap

ALIGNMENTS

RESULT 1
US-09-817-913-12
Sequence 12, Application US/09817913
Patent No. US20020061860A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonfills, Claire
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.115
CURRENT APPLICATION NUMBER: US/09/817, 913
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,157
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 4099
TYPE: DNA
ORGANISM: Human
US-09-817-913-12

Query Match
Best Local Similarity 99.1%; Score 3614.4; DB 10; Length 4099;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3627; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY	1	ATGACCTCAACCGCCGAGATTCCACCAACACGCGGCAAGAGTATGACGAAACCC	60
DB	94	ATGACCTCAACCGCCGAGATTCCACCAACACGCGGCAAGAGTATGACGAAACCC	153
QY	61	CAGCGCCCTCAACCGCCGAGATTCCACCAACACGCGGCAAGAGTATGACGAAACCC	120
DB	154	CAGCGCCCTCAACCGCCGAGATTCCACCAACACGCGGCAAGAGTATGACGAAACCC	213
QY	121	CCCGCTCTATCCCAATCTAGCGAGGTAAAGAAAGCAAAATGAGAGCTCGGC	180
DB	214	CCCGCTCTATCCCAATCTAGCGAGGTAAAGAAAGCAAAATGAGAGCTCGGC	273
QY	181	CAAGCAATGGAAGAGACCTTATGTGGAGCTGCAAGGATGATCTGACCTTGAGGCT	240
DB	274	CAAGCAATGGAAGAGACCTTATGTGGAGCTGCAAGGATGATCTGACCTTGAGGCT	333

Y	241	GAAGACTG6CTG66CACTG6CTTGGTGGTGGATGAGACAGTTAAATGAATTCATTGCCCTC	300
Db	334	GAAGCACTGGCTGGCACTGGCGCTGGTGGTTGGATGAGACAGTTAAATGAATTCATTGCCCTC	393
OY	301	TGGATGACAGCTTCCCGAAGGCCCTGAGCGGCTCATGCCATCAAGAGCACTGATC	360
Db	394	TGGGATGACAGCTTCCCGAAGGCCCTGAGCGGCTCATGCCATCAAGAGCACTGATC	453
OY	361	CAGAGGGGCTCCTGATGCGCTGGCTGCTTCAGGGCCGGTTGCTGAAAAGGACAG	420
Db	454	CAGAGGGGCTCCTGATGCGCTGGCTGCTTCAGGGCCGGTTGCTGAAAAGGACAG	513
OY	421	CTGATGTTGGTTCACAGGCTAGAAATATATTGATCTGATGGAACAACCCAGTACATGAT	480
Db	514	CTGATGTTGGTTCACAGGCTAGAAATATATTGATCTGATGGAACAACAACCCAGTACATGAT	573
OY	481	GAGGAGAACTCCGTGCTCCTAGACAGACCTACGACTAGTTTATCTGCATCCGAATCA	540
Db	574	GAGGAGAACTCCGTGCTCCTAGACAGACCCACGACTAGTTTATCTGCATCCGAATCA	633
OY	541	TACCTCCTGGCTGCTGAGCCCTGAGGCTGTGCTCAGGGCTGAGGCTGAGGCTCCTGGGG	600
Db	634	TACCTCCTGGCTGCTGAGCCCTGAGGCTGTGCTCAGGGCTGAGGCTGAGGCTCCTGGGG	693
OY	601	GCTGAGATCCCGGAATGGCATGGCCATCATTAAGGCTCTCGGACATCACGCCAGCACAGT	660
Db	694	GCTGAGATCCCGGAATGGCATGGCCATCATTAAGGCTCTCGGACATCACGCCAGCACAGT	753
OY	661	CTTATGATGGCTATTTGCAATGTTCAACACAGTGGCTGAGGCCCGCTATGCTCAACAG	720
Db	754	CTTATGATGGCTATTTGCAATGTTCAACACAGTGGCTGAGGCCCGCTATGCTCAACAG	813
OY	721	AAACACCCGCAATCCGAGGGGCTCTTATCTGTAATTTGGATGTGCACACAGGTCAAGAAACA	780
Db	814	AAACACCCGCAATCCGAGGGGCTCTTATCTGTAATTTGGATGTGCACACAGGTCAAGAAACA	873
OY	781	CAGTTCACTTTCGACACAGACCCCACTGCTCTTATCTGCAATCCACCGTACAGCAG	840
Db	874	CAGTTCACTTTCGACACAGACCCCACTGCTCTTATCTGCAATCCACCGTACAGCAG	933
OY	841	GGTAGGTTCTGGCCCCACCTGAAAGGCTCTTAACTGGTCCACACAGTTTGGGCCAAGGC	900
Db	934	GGTAGGTTCTGGCCCCACCTGAAAGGCTCTTAACTGGTCCACACAGTTTGGGCCAAGGC	993
OY	901	CAGGATTTACCAATATGTGCTTGGAAACAAGTGGGGAATGCCGGAATGCTACACTT	960
Db	994	CAGGATTTACCAATATGTGCTTGGAAACAAGTGGGGAATGCTACACTT	1053
OY	961	GCTGCTTCTGACAGTCTGCTGCAATCGCCCTCGAATTCACACCTCAGTGGTCTGT	1020
Db	1054	GCTGCTTCTGACAGTCTGCTGCAATCGCCCTCGAATTCACACCTCAGTGGTCTGT	1113
OY	1021	GTGCTGCTGCAATTTGATGCCCTGCAAGAGGACCCCAAGGGTGAGATGGCCCACTCCG	1080
Db	1114	GTGCTGCTGCAATTTGATGCCCTGCAAGAGGACCCCAAGGGTGAGATGGCCCACTCCG	1173
OY	1081	GCAAGGTTCCGCAAGCTAACCCACCTGCTCAATGGGTCTGCGAAGAGGCAAGCTATCTGT	1140
Db	1174	GCAAGGTTCCGCAAGCTAACCCACCTGCTCAATGGGTCTGCGAAGAGGCAAGCTATCTGT	1233
OY	1141	TCTCTGAGAGGGTGGCTAACCTCCGCGCCCTGAGGTGAAGCGTACAGTCTTGGCTCAC	1200
Db	1234	TCTCTGAGAGGGTGGCTAACCTCCGCGCCCTGAGGTGAAGCGTACAGTCTTGGCTCAC	1299
OY	1201	ACCTCTTGGGAGACCTTGGCCCACTGCTGAGATCACTGTGATGCCCTGCGCGAGTGC	1260
Db	1294	ACCTCTTGGGAGACCTTGGCCCACTGCTGAGATCACTGTGATGCCCTGCGCGAGTGC	1353
OY	1261	CAGGCTTCAGTTTCTGCTGTGCTGGAACCCCTGAGCCCTTCTGGGAAGTCTTGTGAGA	1320
Db	1354	CAGGCTTCAGTTTCTGCTGTGCTGGAACCCCTGAGCCCTTCTGGGAAGTCTTGTGAGA	1413
OY	1321	TCAACTGAGACCTGAGAGGGGACACATGAGAGGAGGCAATGTGAGAGAGAGGAGAG	1380

[illegible]

Db 2494 GACCCACACCCCTGCTGACCCCTGACGCCCCCACTATGAGGGCCCTGGCCAAATC 2553
QY 2461 ACTGAGACCATCAGTCCATGCGAGATATGCGGCACCTTACGGGTATGAAAGTAA 2520
Db 2554 ACTGAGACCATCAGTCCATGCGAGATATGCGGCACCTTACGGGTATGAAAGTAA 2613
QY 2521 GACAGAGAAGGACCTCCAGTCTTAAGTTGGTCAACAAGAAAGGACCCCAACCAAGCAAA 2580
Db 2614 GACAGAGAAGGACCTCCAGTCTTAAGTTGGTCAACAAGAAAGGACCCCAACCAAGCAAA 2673
QY 2581 CCTAGGTAGCTGAGCGGATGACCAACAGAAAAAGAAAGTCTTGGAAAGCAGGCTAGGG 2640
Db 2674 CCTAGGTAGCTGAGCGGATGACCAACAGAAAAAGAAAGTCTTGGAAAGCAGGCTAGGG 2733
QY 2641 AAAGTCACTTGGGATCATTTGGGGAGAGTCCACTCCAGGCCAGACTTAATCTCAGAGCA 2700
Db 2734 AAAGTCACTTGGGATCATTTGGGGAGAGTCCACTCCAGGCCAGACTTAATCTCAGAGCA 2793
QY 2701 GCTGTGGTGGCCCTCAGTCAGAGCAGCCCTCAGAGGAGCCAGAGGGGGAGCCCTGTG 2760
Db 2794 GCTGTGGTGGCCCTCAGTCAGAGCAGCCCTCAGAGGAGCCAGAGGGGGAGCCCTGTG 2853
QY 2761 GCCCAGACCAATTTCTGAGGAGCAGCCATTGGGGAGCCATGCTGGGCCAGACCACTCAGAG 2820
Db 2854 GCCCAGACCAATTTCTGAGGAGCAGCCATTGGGGAGCCATGCTGGGCCAGACCACTCAGAG 2913
QY 2821 GAGGCTGTGGGGGAGGAGCCACTCCGAGACAGCACTCAGAGGAGTGTGGGAGGAGCC 2880
Db 2914 GAGGCTGTGGGGGAGGAGCCACTCCGAGACAGCACTCAGAGGAGTGTGGGAGGAGCC 2973
QY 2881 ATTCTGACCAAGACCACTCAGAGGAGTGTGGGGGAGCCAGGCTGGCCAGACTAC 2940
Db 2974 ATTCTGACCAAGACCACTCAGAGGAGTGTGGGGGAGCCAGGCTGGCCAGACTAC 3033
QY 2941 TCAGAGGAGGCTGAGGAGGAGTACACTGGCCAGACCACTCTGAGAGGACCCATGTGAG 3000
Db 3034 TCAGAGGAGGCTGAGGAGGAGTACACTGGCCAGACCACTCTGAGAGGACCCATGTGAG 3093
QY 3001 GGAGCCCACTGAGACCACTCAGAGAGGAGTCCAGAGGGGAGCCAGGACTGATCCAA 3060
Db 3094 GGAGCCCACTGAGACCACTCAGAGAGGAGTCCAGAGGGGAGCCAGGACTGATCCAA 3153
QY 3061 ACTGCTCTAGCCTGAGACAGACCAACCCGCCCACTCAGTGTGAGGAGAACT 3120
Db 3154 ACTGCTCTAGCCTGAGACAGACCAACCCGCCCACTCAGTGTGAGGAGAACT 3213
QY 3121 ACACCCAGATATCTCCAGTACACTGATTTGGAGTCTCAGAGACCTTGGAGCTAGGAGC 3180
Db 3214 ACACCCAGATATCTCCAGTACACTGATTTGGAGTCTCAGAGACCTTGGAGCTAGGAGC 3273
QY 3181 GAATCTCAGGAGGAGCTCAGATCTCAGAGCCCGAGAGAGAGAACTACTAGGAGAGCA 3240
Db 3274 GAATCTCAGGAGGAGCTCAGATCTCAGAGCCCGAGAGAGAGAACTACTAGGAGAGCA 3333
QY 3241 GCTGAGAGTCAAGACATGCTGATTTGATGAGGAGATCTAGGGGAGCTCAGTAT 3300
Db 3334 GCTGAGAGTCAAGACATGCTGATTTGATGAGGAGATCTAGGGGAGCTCAGTAT 3393
QY 3301 CAGGCAATATTTATGCTGTGACACCACTGCGCTGGTGTCCCACTTTGGTGGCAGTATGC 3360
Db 3394 CAGGCAATATTTATGCTGTGACACCACTGCGCTGGTGTCCCACTTTGGTGGCAGTATGC 3453
QY 3361 CCCATACCTCAGAGGAGCTAGAGGTAGACCAACCTTGGGGAGCTGGGAGCAATCCAA 3420
Db 3454 CCCATACCTCAGAGGAGCTAGAGGTAGACCAACCTTGGGGAGCTGGGAGCAATCCAA 3513
QY 3421 GAGAAATGGGTGTGTCTCTTGTCTATCAGTCTACTGTGTCTCTTACATCAATAGGCAC 3480
Db 3514 GAGAAATGGGTGTGTCTCTTGTCTATCAGTCTACTGTGTCTCTTACATCAATAGGCAC 3573
QY 3481 ATGCTCCAAACCATGGAATTTCTGGACACCCGCTGCTCCTCAGCTACATGAGCCTGTCA 3540
Db 3574 ATGCTCCAAACCATGGAATTTCTGGACACCCGCTGCTCCTCAGCTACATGAGCCTGTCA 3633

QY 3541 GCCTGGTCTTACTACTGTGAGGCTTGTGTCACACACAGGCTCTCTAGATGGAAGAC 3600
Db 3634 GCCTGGTCTTACTACTGTGAGGCTTGTGTCACACACAGGCTCTCTAGATGGAAGAC 3693
QY 3601 ATCGGCCACAGAACAGTTTGGGGAGGATGATGCCCAACCCACACTTA 3648
Db 3694 ATCGGCCACAGAACAGTTTGGGGAGGATGATGCCCAACCCACACTTA 3741

RESULT 2
US-09-817-538-12
Sequence 12, Application US/09817538
Patent No. US20020137162A1
GENERAL INFORMATION:
APPLICANT: LI, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
FILE REFERENCE: 106101.144
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 4099
TYPE: DNA
ORGANISM: Human
US-09-817-538-12

Query Match 99.1%; Score 3614.4; DB 10; Length 4099;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3627; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGACCTCAACCGGCGAGGATTCACACACAGCAGAGAGTGAAGGCGAAGCC 60
Db 94 ATGACCTCAACCGGCGAGGATTCACACACAGCAGAGAGTGAAGGCGAAGCC 153
QY 61 CAGTGGCCCTCAGAGACTCCAGTGTCACTTGGAAAGCAATTTAAAAAGGAGCGGT 120
Db 154 CAGTGGCCCTCAGAGACTCCAGTGTCACTTGGAAAGCAATTTAAAAAGGAGCGGT 213
QY 121 CCGGCTCTATCCCAATCTAGCGAGGTAAAGAAAGCAAAATGAAAGACTGCGC 180
Db 214 CCGGCTCTATCCCAATCTAGCGAGGTAAAGAAAGCAAAATGAAAGACTGCGC 273
QY 181 CAAGCAATGGAAGAGACTTAATCGTGGGAGTCAAGAGGATGATGAACTTGAAGCT 240
Db 274 CAAGCAATGGAAGAGACTTAATCGTGGGAGTCAAGAGGATGATGAACTTGAAGCT 333
QY 241 GAAGCACTGGGCGAGCTGGCTTGGTGTGATGAGCACTTAATGAAATTCATTCCTC 300
Db 334 GAAGCACTGGGCGAGCTGGCTTGGTGTGATGAGCACTTAATGAAATTCATTCCTC 393
QY 301 TGGATGACAGCTTCCCGAGAGGCCCTGAGCGGCTCCATGCCATCAAGAGCACTGATC 360
Db 394 TGGATGACAGCTTCCCGAGAGGCCCTGAGCGGCTCCATGCCATCAAGAGCACTGATC 453
QY 361 CAGAGGAGGCTCCTGATGCTGGGCTGCTTCAAGGCGGCTTGTCTGCAAAAGAGAG 420
Db 454 CAGAGGAGGCTCCTGATGCTGGGCTGCTTCAAGGCGGCTTGTCTGCAAAAGAGAG 513
QY 421 CTGATGTTGCTTCAAGGCTGAAATATATTGATCTGATGGAAGAAACCCAGTACATGAAT 480
Db 514 CTGATGTTGCTTCAAGGCTGAAATATATTGATCTGATGGAAGAAACCCAGTACATGAAT 573
QY 481 GAGGAGAACTTCGCTCTTCAAGAGCACTAAGCACTGATTTATCTGATCCGAATCTCA 540
Db 574 GAGGAGAACTTCGCTCTTCAAGAGCACTAAGCACTGATTTATCTGATCCGAATCTCA 633

Db 2794 GCTGTGTTGGCTCTACCTAGGACCAAGCCCTCAGAGGCGCACAGGGGGAGCCACTCTG 2853
Qy 2761 GCCAGACCAATTTGTGAGGACGATTTGGGGAGCCATGCTGGGCGACAGCACTCAGAG 2820
Db 2854 GCCAGACCAATTTGTGAGGACGATTTGGGGAGCCATGCTGGGCGACAGCACTCAGAG 2913
Qy 2821 GAGGCTGTGGGGGAGGACCTCCGAGACAGCACTCAGAGGAGGAGCTGTGGGAGAGCC 2880
Db 2914 GAGGCTGTGGGGGAGGACCTCCGAGACAGCACTCAGAGGAGGAGCTGTGGGAGAGCC 2973
Qy 2881 ATTCTGACCAAGACCACTCAGAGAGTCTGTTGGGGAGCCAGCTGTGGGCGACACTAC 2940
Db 2974 ATTCTGACCAAGACCACTCAGAGAGTCTGTTGGGGAGCCAGCTGTGGGCGACACTAC 3033
Qy 2941 TCAGAGAGGCTGTAGAGAGCTACACTGTGGCCAGACCACTCTGGAGGAGCCATGAG 3000
Db 3034 TCAGAGAGGCTGTAGAGAGCTACACTGTGGCCAGACCACTCTGGAGGAGCCATGAG 3093
Qy 3001 GAGGCCACACTGAGACCACTACACTCAGAGAGGCTCCAGGGGCGACCGAGCTGATCCA 3060
Db 3094 GAGGCCACACTGAGACCACTACACTCAGAGAGGCTCCAGGGGCGACCGAGCTGATCCA 3153
Qy 3061 ACCTCTTACCTCTGAGACCAAGACCACTACACTGATTTGGGAGTCTCAGAGCTGTGAGG 3120
Db 3154 ACCTCTTACCTCTGAGACCAAGACCACTACACTGATTTGGGAGTCTCAGAGCTGTGAGG 3213
Qy 3121 ACACCCAGATATCTCCAGTACACTGATTTGGGAGTCTCAGAGCTGTGAGGAGTCTGAG 3180
Db 3214 ACACCCAGATATCTCCAGTACACTGATTTGGGAGTCTCAGAGCTGTGAGGAGTCTGAG 3273
Qy 3181 GAATCTCAGAGGAGGCTCAGAACTCAGAGGCGCCAGAGAGAGAACTACTAGAGAGGCA 3240
Db 3274 GAATCTCAGAGGAGGCTCAGAACTCAGAGGCGCCAGAGAGAGAACTACTAGAGAGGCA 3333
Qy 3241 GCTGAGAGTAGAGCATGAGGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 3300
Db 3334 GCTGAGAGTAGAGCATGAGGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 3393
Qy 3301 CAGGCAATATTTATGCTGTGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Db 3394 CAGGCAATATTTATGCTGTGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3453
Qy 3361 CCCATACCTCAGAGGAGGCTCAGAGCTAGAGCTAGAGCTAGAGCTAGAGCTAGAGCT 3420
Db 3454 CCCATACCTCAGAGGAGGCTCAGAGCTAGAGCTAGAGCTAGAGCTAGAGCTAGAGCT 3513
Qy 3421 GAGAAATGGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Db 3514 GAGAAATGGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3573
Qy 3481 ATGCTCCACACCACTGAGAAATTTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3574 ATGCTCCACACCACTGAGAAATTTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3633
Qy 3541 GCTGTGTTACTACTGCTCAGGCTATGCTCAGACCAAGGCTCTCTAGATGTGAAGAC 3600
Db 3634 GCTGTGTTACTACTGCTCAGGCTATGCTCAGACCAAGGCTCTCTAGATGTGAAGAC 3693
Qy 3601 ATGCCCAACCAAGAAATTTGGGAGGATATGCCCAACCACTAA 3648
Db 3694 ATGCCCAACCAAGAAATTTGGGAGGATATGCCCAACCACTAA 3741

RESULT 3

US-09-976-280A-1
; Sequence 1, Application US/09976280A
; Patent No. US2002011517A1
; GENERAL INFORMATION:
; APPLICANT: Zhi, Zhimin
; TITLE OF INVENTION: Regulation of Human Histone Deacetylase
; FILE REFERENCE: 004974.00590
; CURRENT APPLICATION NUMBER: US/09/976, 280A
; CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/239,928
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-976-280A-1

Query Match 9.5%; Score 346; DB 10; Length 2022;
Best local similarity 60.4%; Pred No. 4.9e-95;
Matches 571; Conservative 0; Mismatches 375; Indels 0; Gaps 0;

Qy 319 GAAGCCCTGAGCGGCTCCATCCATCAAGAGCACTATCCAGAGGAGGCTCTAGAT 378
Db 76 GAGGCTCTGAGCGGCTGAGCGGACGACCCCTGAGTCCGCTCGGAGCGCGGCTGGAACAG 135
Qy 379 GCTGCGTGTCTTTCAGGCGCGGTTTCTGTAAGAGAGCTGATGTTGTTCAACAG 438
Db 136 AGGTGTCTGCGGTGTCTGAGCCCGCAGAGCGCTCGGAAGAGAGCTGCGCTGTGTACAGC 195
Qy 439 CTAGAAATATATGATGATGTAAGAAACCACTCATGATGAGGAGAGCACTCCGTTC 498
Db 196 CAGAGTATATATCTCTGCTGAGGAGACCCAGGCTCTAGGCAAGGAGAGCTGACAGCG 255
Qy 499 CTAGAGACACCTTACGACATGATTTATGATCCGAACTCACTCTGCTGCTGCTGCTG 558
Db 256 CTGTCCGAGACATTTGAGCGGCTGATCTGATCTTCAACCGAGTACTCTTACTGCGCGGCTG 315
Qy 559 GCTTCAGGCTCTGCTCAGGCTGAGGTGAGTGGGCTGCTGAGTCCGGAATGCG 618
Db 316 GCGCGAGGCGCTGAGCTGAGGTGAGTGGGCTGCTGAGTCCGGAATGCG 375
Qy 619 ATGCCATCATATGAGGCTCTGCTGAGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAG 678
Db 376 CTGCGCTGCTGAGGCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 435
Qy 679 ATGTTCAACCACTGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 738
Db 436 GTGTTCAACCACTGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 495
Qy 739 GTCTTATGATGATTTGAGGAGTGCACAGGCTCAAGAGAACTGCTGCTGAGGAG 798
Db 496 ATCTGCTGAGGAGTGCACAGGCTCAAGAGAACTGCTGCTGAGGAG 555
Qy 799 GAGCCCACTGCTTATTTCTTCCATCCAGGCTCAGAGGAGGAGGAGGAGGAGGAGGAGG 858
Db 556 GAGCCCACTGCTTATTTCTTCCATCCAGGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 615
Qy 859 CTGAAGGCTCTTATTTCTTCCATCCAGGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 918
Db 616 CTGCGAGAGTCAAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 675
Qy 919 GTGCTTGAACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 978
Db 676 CTGCTTGAACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 735
Qy 979 CTGCTTGAACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1038
Db 736 CTGCTTGAACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 795
Qy 1039 GCGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1098
Db 796 TCAGGCATCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 855
Qy 1099 ACCACCTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1158
Db 856 ACACAGCTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 915
Qy 1159 AACCTCCGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1218
Db 916 CACCTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975

QY 1219 TCCCCCATGCTGGAGTCACCTGGTGGCCCCCTGCCGGAGTGGCCAGG 1264

Db 976 GCCCCACCCCTGTGAGGGCCAATGGCGCCATGTCAAGAGTGGCAGG 1021

RESULT 4

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US-09-983-965-5409
: Sequence 5409, Application US/09983965
: Patent No. US20020137160A1
: GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Nengping
: APPLICANT: Byatt, John C.
: APPLICANT: Mathialagan, Nagappan
: TITLE OF INVENTION: NOCTIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
: FILE REFERENCE: 37-21(10297)C
: CURRENT APPLICATION NUMBER: US/09/983, 965
: CURRENT FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: US 09/465,231
: PRIOR FILING DATE: 1999-12-15
: PRIOR APPLICATION NUMBER: US 60/113,678
: PRIOR FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 5912
: SEQ ID NO 5409
: LENGTH: 418
: TYPE: DNA
: ORGANISM: Bos taurus
: FEATURE:
: OTHER INFORMATION: Clone ID: 44-LIB34-014-Q1-E1-C8
: US-09-983-965-5409

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Query Match	6.28;	Score 226.6;	DB 10;	Length 418;
Best Local Similarity	74.58;	Pred. No. 8,1e-59;		
Matches 321;	Conservative 0;	Mismatches 89;	Indels 21;	Gaps 2

QY	3109	GTGGAGGGAACCTACACCCCAATATCTCCAGTACAGTATGGGAGTCTCAGACCTTG	316
Db	3	GTGGAGGAGCCACACCCCGACATCCCTGTAAAGTGAATGGCAAACTCAGAAATACTG	62
QY	3169	GAGCTAGGACAGCAATCTCAGGAGGGGCTCAGAAATCTCAGAGGCCCAAGAGAGAGAACTTA	3228
Db	63	GACCTAGATAGCACAGCACTCAGAGGCCCTCAGA-----AGAGGAAGAGCTA	107
QY	3229	CTAGAGAGGAGCAGCTGGAGGTCAGACATGGCTGATTGCAATCTATGACGAGATCTAGG	3288
Db	108	CTAGAGAGGAGGAGCTGGAGGTCAGAGACAAATGTAGTAGTCCAGTGGAGGTCCTTTGGA	167
QY	3289	GGCC-----TCACGATACAGGCCCTATTTTATGTGTGACACCACTGGCCCTGGTGTCC	334
Db	168	GATCATGCTGACACTGAGAGAGGTATGTTTATGCCGTAAGACCACTGCTTTGGTGTCTT	227
QY	3343	CATTGGTGGCAGTATGCTCCCATACCTTGACAGAGGCTTAGACGTAGCCCACTTGTGGG	340
Db	228	CATTGGGGGAGATGCCCCATCTACTAGACAGGGCTGAATGTATACCAACTTGTGAG	287
QY	3403	GACTGTGGAAACAATCCAGAGAAATTTGGGTGTCTCTGTGTATCAGSTCTACTGTGT	346
Db	288	GACTGTGGAAACCTCCAGGAATCTGGGTGTGTCTGTGTATCAATGTCTACATGCCGT	347
QY	3463	CGTTACATCAATGGCCACATGCTCCCAACACCATGGAATTTGGAACCCGCTGCTCCG	3522
Db	348	CGTTACATCAACGCTCATATGCTCTCAGACACCATGAATGTTGAGACACCACTAATATCTC	407
QY	3523	AGCTACATCGA	3533
Db	408	AGCTATGCCGA	418

RESULT 5
US-09-817-913-14
; Sequence 14, Application US/09817913

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? Patent No. US20020061860A1
? GENERAL INFORMATION:
? APPLICANT: Li, Zhongmei
? APPLICANT: Bonfilis, Claire
? TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
? FILE REFERENCE: 106101.145
? CURRENT APPLICATION NUMBER: US/09/817,913
? CURRENT FILING DATE: 2001-03-26
? PRIOR APPLICATION NUMBER: US 60/192,157
? PRIOR FILING DATE: 2000-03-24
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 14
? LENGTH: 3131
? TYPE: DNA
? ORGANISM: Human
? US-09-817-913-14

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Query Match	5.8%;	Score 210.6;	DB 10;	Length 3131;
Best Local Similarity	58.8%;	Pred: No. 1.5e-53;		
Matches 426;	Conservative	0;	Mismatches 284;	Indels 15; Gaps 3

QY	1694	ACTTTGACATCCATATATATCTGCCCCAGTACCTTGCTGTGACACAGCTTGCCACTGGCC	1753
Db	1966	ACACTGTACACCATCTGGAGTATGAGCTTTCATCTCCATATGACAGCCCGCTGGGGCGGTGGCA	2022
QY	1754	CTGCCTGACCGCTGTGTGGAGGCTGTGCCTCTAGGAGAGGTCTGTAAATGTGTCTGCTGTGG	1813
Db	2026	GTGTCACTGACCTTGCCCTTCAAAAGTGGCTTCTCTGACCTTAAAGAAATGTGTCTGCTGTGG	2088
QY	1814	TGCGTCCCCCAGAGACACCCAGACAGAGATGACCTTGGCGGTTTTTGTCTTTTCAACT	1873
Db	2086	TGCGGGCCCCCAGAGACACCATCATGATCTATTCAACAGCCATGGGCTTCTGCTTCTTCAACT	2145
QY	1874	CTGTGCGCTGTGGCTGCTCG-----CCATGCCACAGACTATCATGTGGGCGTGGCCCTTACGGA	1927
Db	2146	CAGTGGCCCATCGCCTGGCCGGCAGGTGCAACAGACAGACGAAGGCCACAGAGGCCACACAGA	2209
QY	1928	TCTCTGATTTGTGATTTGGGATGTCCACACAGGTAATGGAATCAGACATGTTTAGAGATG	1988
Db	2206	TCTCATTTGTGTAGCTGGGACGTGACCATCATGCGCAACGGCACCCAGCAAACTTCTTACCAAG	2265
QY	1988	ACCCCAAGTGTCTATATGTGTCCCTTGACCGGCTATGATCATATGGACCTTCTTCCCCATGG	2044
Db	2266	ACCCCAAGTGTCTCTACATCTCCCTTGCAATGCCATGACGACGGCAACTCTTCCCGGGGA	2322
QY	2048	GGATATGAGGGGTGCCAGCAGCCAGATGTGGCGCGGGCGCGGACAGAGGCTTCAACCGTCACAG	2107
Db	2326	GTGGGGCTGTGTGATATGAGGTATAGGGGCTGGCAGCGGTGAGGGCTTCAATATGTATGTGGCT	2388
QY	2108	TGGC---ATGGAAACGGGCCCCGACATGGGTGATGTGCTAGCTATACCTATAGCTCTGGCATTCGC	2166
Db	2386	GGCGTGGAGGCTGTGACACCCCCCAGTGGGGGATCTGTAATACCTGGCTCTTTCAGAGATAG	2445
QY	2165	TGTGTCTTCCCATTTGCTACGATGTTTAAACCCAGAACTGTGTCTGTCTCTACCTGGCTTTG	2222
Db	2446	TCTGTAGCGCCCATCGCCCGAGAGTTTCTCTCCAGCACTATAGCTCTGTGTCTCTCCGGATTTG	2505
QY	2225	ATGTGTGACGGGGGGATTCGG-----CTGGGGGCTGTCCAGGTGTGCACCTATAGGGTTATG	2278
Db	2506	ATGTGTGTGAGGGGTACCCCGGCCCCCAGCTGAGTGGCTTACATATGTTTCTGTCCAAATGTTTTG	2565
QY	2279	CCCACCTACACCACTGTGATGTGGCGCTTGGCATGTGGCCGCAATATCTTATTCCTAGAG	2338
Db	2566	GATTCATATGACGACCAACTATATGAACCTGGCAGAGAGCGCAGTGTGCTGGCTTTGGAGG	2625
QY	2339	GTGGCTATTAACCTGACATTCATCTCAGAGTTCATATGGCTGCTGTGCATCTGCTCTCTTG	2398
Db	2626	GTGGCCATATGACCTACAGCCATCTGTATACGCGCTGTAGAGCGCTGTGTGGCTCTCTTCTGG	2685
QY	2399	GAGAC 2403	

Db 3670 CTGATGGCCCTGGGCTGGCGGCCGATGTCTCTGGCCCTCGAGGAGGCGCACGACCTGCAC 3729

QY 2356 TCCATCTCAGAGTCCATGGCTGGCCCTGCACCTGCTCCCTCTTGGAGAC 2403

Db 3730 GCCATTGGCGAGCGCTCGGAAGCATGTGTCTCTGCTGCTGGCGAAC 3777

RESULT 8

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US-09-817-913--8
; Sequence 8, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OR INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8459
; TYPE: DNA
; ORGANISM: Human
; US-09-817-913--8

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Query Match	5.3%;	Score 192.4;	DB 10;	Length 8459;
Best Local Similarity	59.4%;	Pred. No. 8.5e-48;		
Matches 385;	Conservative 0;	Mismatches 251;	Indels 12;	Gaps 3

Dy 2356 TCATCTCAGAGTCATGGCTGCGTGCACCTCCCTCCTTTGAGAC 2403
||| | ||| ||| ||| ||| ||| ||| |||
Db 3730 GCCATTGCGAGCGCTCGAAGCATGTGTTTCGCCCTGCGGGAAAC 3777

RESULT 9

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US-09-817-538-8
; Sequence 8, Application US/09817538
; Patent No. US20020137162A1
GENERAL INFORMATION:
APPLICANT: LI, Zumei
APPLICANT: Bonifils, Claire
APPLICANT: Bestleman, Jeffrey
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
TITLE OF INVENTION: Deacetylase Isoforms
FILE REFERENCE: 106101.144
CURRENT APPLICATION NUMBER: US/09/817,538
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,157
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8459
;
; TYPE: DNA
; ORGANISM: Human
; US-09-817-538-8

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Query Match	5.3%;	Score 192.4;	DB 10;	Length 8459;
Best Local Similarity	59.4%;	Pred. No. 8.5e-48;		
Matches 385;	Conservative 0;	Mismatches 251;	Indels 12;	Gaps 3;

RESULT 12
US-09-817-538-10
Sequence 10, Application US/09817538
Patent No. US2002013162A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
FILE REFERENCE: 106101.144
CURRENT FILING DATE: 2001-03-26
PRIORITY FILING DATE: 2000-03-24
PRIORITY FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 2233
TYPE: DNA
ORGANISM: Human
US-09-817-538-10

Query Match 4.8%; Score 173.6; DB 10; Length 2233;
Best Local Similarity 60.0%; Pred. No. 2.7e-42;
Matches 372; Conservative 0; Mismatches 224; Indels 24; Gaps 4;

1777 GTGCTCAGAGAGAGTCTGATGATGCTGTGTGTCGTCGCCAGAGACGACGCA 1836
1227 GTGCTCAGAGAGAGTCTGATGATGCTGTGTGTCGTCGCCAGAGACGACGCA 1286
1837 GAGCAGAGTCAAGCTTGGGTTTTCCTTTTCAACCTGTGTGCTGTGCTGTGCT 1896
1287 GAGCAGAGTCAAGCTTGGGTTTTCCTTTTCAACCTGTGTGCTGTGCTGTGCT 1346
1897 GCCAGACTATCAGTGGGATGCTTACGATCCGATTTGGATTTGGATTTCCACAC 1956
1347 CTACAG---CAGAACTTAAAGTGGGCAAGTCCATGCTGAGTGGGCAATTCACAT 1403
1957 GGTATGGAAGTCAAGCTTGGGTTTTCCTTTTCAACCTGTGTGCTGTGCTGTGCT 2016
1404 GGCATGAGCAGCAGAGGCTTCTATATATACCCCTCTGTCTGTCTGTCTGTCT 1463
2017 CGCTATGATCATGACCTTTTCCCATGAGGAGTGAAGGTCGACGACGATCGGC 2076
1464 CGCTATGATCATGACCTTTTCCCATGAGGAGTGAAGGTCGACGACGATCGGC 1517
2077 CGGCTGAGGAGCAGGCTTACCGTCAACGTCGATGGAACG-----GCCCGC 2127
1518 GAGAGACGAGCAGGCTTACCGTCAACGTCGATGGAACG-----GCCCGC 1577
2128 ATGAGTGAAGTCAAGCTTGGGTTTTCCTTTTCAACCTGTGTGCTGTGCTGTGCT 2187
1578 ATGAGTGAAGTCAAGCTTGGGTTTTCCTTTTCAACCTGTGTGCTGTGCTGTGCT 1637
2188 TTTTAAACCAAGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2241
1638 TTTTAAACCAAGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1697
2242 CCGCTGAGGAGCAGGCTTACCGTCAACGTCGATGGAACG-----GCCCGC 2301
1698 CCGCTGAGGAGCAGGCTTACCGTCAACGTCGATGGAACG-----GCCCGC 1757
2302 GGCCTTCCAGTGGGCTTACCGTCAACGTCGATGGAACG-----GCCCGC 2361
1758 ACCCTGAGGAGCAGGCTTACCGTCAACGTCGATGGAACG-----GCCCGC 1817
2362 TCAGATGATGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2381
1818 TGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1837

RESULT 13
US-10-173-539-5
Sequence 5, Application US/10173539
Publication No. US20030059812A1
GENERAL INFORMATION:
APPLICANT: Richon, Victoria
APPLICANT: Zhou, Xianbo
APPLICANT: Rifkind, Richard A.
TITLE OF INVENTION: HDAC9 Polypeptides and Polynucleotides
FILE REFERENCE: 3254.1000-003
CURRENT FILING DATE: 2002-06-14
PRIORITY FILING DATE: 2001-06-14
PRIORITY FILING DATE: 2001-06-14
PRIORITY FILING DATE: 2001-06-14
PRIORITY FILING DATE: 2001-08-10
PRIORITY FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 3054
TYPE: DNA
ORGANISM: Homo sapiens
US-10-173-539-5

Query Match 4.3%; Score 155.2; DB 9; Length 3054;
Best Local Similarity 54.0%; Pred. No. 1.3e-36;
Matches 388; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

1694 ACTTGACATCAATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1753
2228 ACAGTGAACCAATTTGGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2287
1754 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1813
2288 GTGCTCATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2347
1814 TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1873
2348 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2407
1874 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1933
2408 CAGTTGATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2464
1934 TTTGATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1993
2465 TTTGATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2524
1994 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2053
2525 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2584
2054 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2113
2585 CCGCAATTAAGTGTGGAACAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2644
2114 GGAAC---GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2170
2645 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2704
2171 TTTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2230
2705 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2764
2231 CACGGGAGGAG---TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2284
2765 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2824
2285 TCACCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2344

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Db      2825 TGACGAGCAATGATGACATTTGGCTATGACGCTGTGTGGCTCTATAGAGAGAC 2884
QY      2345 ATAACCTGACATTCATCTCAGAGTCCATGGCTGCTGCATCGCTCCCTCTGAGAGA 2402
Db      2885 ATGATCTCAGACGACATCTGTGATGATCAGAGAGCCTGTGTAATAGCCCTCTAGAGAA 2942
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RESULT 14

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US-10-072-094-97
; Sequence 97, Application US/10072094
; Publication No. US2003002538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145U51
; CURRENT APPLICATION NUMBER: US/10/072,094
; PRIORITY FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3183)
US-10-072-094-97
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Query Match 4.3%; Score 155.2; DB 9; Length 3186;

Best Local Similarity 54.0%; Pred. No. 1.3e-36;

Matches 388; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

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QY      1694 ACTTTGACTCCATCTATATCTGCCCACTTCCTGCTGACAGCTTGCACATGCGC 1753
Db      2360 ACAGTGACACCATTTGGAATGAGCTACACGTGCTGGTGGCAGCGCATGCTGTGCT 2419
QY      1754 CTGCTGCGCCGCTGCTGAGAGGCTGTCTCAGAGAGGTTGTAATGCTGCTGTGG 1813
Db      2420 GTGTCTCATGAGCTGGCTTCCAAAGTGCTCAGAGAGCTGAAGAAATGGCTTCTGTG 2479
QY      1814 TGGTCCCCCAGAGACCAAGCAGAGACGATGACGCTTGGGATGCGCTACAGATCTGA 1933
Db      2480 TGAAGGCCCTGAGCAGCTGAGAGAAATCCACAGCCATGAGGCTTGTCTTTTAAAT 2539
QY      1874 CTGTGCTGTGGCTGCTGCGCATGCGCAGACTATCATGAGGATGCGCTACAGATCTGA 1933
Db      2540 CAGTTGCATTAACCGC---CAATACCTTGAGAGACCACTAAATATAGCAAGATATTGA 2596
QY      1934 TTGTGATTTGGATGTCTCCACACCGATATGGAATGGAATCTGACATGTTGAGATGACCCA 1993
Db      2597 TTGTAGATCTGAGATGTTTACCATGAGAAAGGTACCCAGAGGCTTTTATGCTGACCCA 2656
QY      1994 GTTGTATATATGTCTCCCTGACACCGCTATATATATGACGACTTCTTCCCATGGGAGATG 2053
Db      2657 GCATCTGTAGATTTTCACTCCATGCTATATGAAAGGAACCTTTTCTCGGACGTGAG 2716
QY      2054 AGGCTGCCAGCAGCAGATCGCGGCGGCTGCGGACAGAGCTTACCGCTCAAGCTGAGCAT 2113
Db      2717 CCCCCAATGAGGTGGAACAGGCGCTTGAAGAGGATGCAATATATATATGCTGACCCCA 2776
QY      2114 GGAAC---GGGCCCGCAGTGGGTGATGCTACTACTAGCTGCTGCGCTGCGCTGCGC 2170
Db      2777 GTGGCCTTGATCTCCCATGGAGATGTTGATGATCTTGAAGCACTTCAGACCATCTGGA 2836
QY      2171 TTCCCATTTGCTGCTGAGTTTAACCCAGAAATGTGTGCTGTGCTCAGCTGCGCTTATCTGTG 2230
Db      2837 AGCTGTGGCCAAAGATTGATTCAGACAAATGCTTATGATCTGTGATGATGATCAT 2896
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QY      2221 CACGGGGGGA-----TCGCTGAGGGGCTGCCAGGTGTACACTGAGGCTTATGCCACC 2284
Db      2897 TGAAGGCGACACCCCTCTCTTAGAGAGGGTACAAAGTACAGGCCAAATATTTTGTCAAT 2956
QY      2285 TCACCCACTGTGTATGAGGCGCTTGGCAGTGGCGCATTTATCTTATCCATAGAGGTGGCT 2344
Db      2957 TGACGACCAATTTGATGACATTTGCTGATGAGACGTGTGGTGTGGCTCTAGAGAGAGAC 3016
QY      2345 ATAACCTGACATTCATCTCAGAGTCCATGGCTGCTGCATGCTGCTCTCTCTTCTGAGAGA 2402
Db      3017 ATGATCTCAGACGACCATCTGTGATGATGATCAGAGAGCCTGTGTAAATGCTTCAAGAGAA 3074
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RESULT 15

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US-10-173-539-1
; Sequence 1, Application US/10173539
; Publication No. US20030059812A1
; GENERAL INFORMATION:
; APPLICANT: Richon, Victoria
; APPLICANT: Zhou, Xianbo
; APPLICANT: Rifkind, Richard A.
; APPLICANT: Marks, Paul A.
; TITLE OF INVENTION: HDAC9 Polypeptides and Polynucleotides
; FILE REFERENCE: 3254.1000-003
; CURRENT APPLICATION NUMBER: US/10/173,539
; PRIORITY FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,173
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/311,686
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/316,995
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-173-539-1
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Query Match 4.3%; Score 155.2; DB 9; Length 3186;

Best Local Similarity 54.0%; Pred. No. 1.3e-36;

Matches 388; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

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QY      1694 ACTTTGACTCCATCTATATCTGCCCACTTCCTGCTGACAGCTTGCACAGCTTGCACATGCGC 1753
Db      2360 ACAGTGACACCATTTGGAATGAGCTACACGTGCTGGTGGCAGCGCATGCTGTGCT 2419
QY      1754 CTGCTGCGCCGCTGCTGAGAGGCTGTCTCAGAGAGGTTGTAATGCTGCTGTGG 1813
Db      2420 GTGTCTCATGAGCTGGCTTCCAAAGTGCTCAGAGAGCTGAAGAAATGGCTTCTGTG 2479
QY      1814 TGGTCCCCCAGAGACCAAGCAGAGACGATGACGCTTGGGATGCGCTACAGATCTGA 1933
Db      2480 TGAAGGCCCTGAGCAGCTGAGAGAAATCCACAGCCATGAGGCTTGTCTTTTAAAT 2539
QY      1874 CTGTGCTGTGGCTGCTGCGCATGCGCAGACTATCATGAGGATGCGCTACAGATCTGA 1933
Db      2540 CAGTTGCATTAACCGC---CAATACCTTGAGAGACCACTAAATATAGCAAGATATTGA 2596
QY      1934 TTGTGATTTGGATGTCTCCACACCGCTATATGGAATGGAATCTGACATGTTGAGATGACCCCA 1993
Db      2597 TTGTAGATCTGAGATGTTTACCATGAGAAAGGTACCCAGAGGCTTTTATGCTGACCCCA 2656
QY      1994 GTTGTATATATGTCTCCCTGACACCGCTATATATATGACGACTTCTTCCCATGGGAGATG 2053
Db      2657 GCATCTGTAGATTTTCACTCCATGCTATATGAAAGGAACCTTTTCTCGGACATGAG 2716
QY      2054 AGGCTGCCAGCAGCAGATCGCGGCGGCTGCGGACAGAGCTTACCGCTCAAGCTGAGCAT 2113
Db      2717 CCCCCAATGAGGTGGAACAGGCGCTTGAAGAGGATGCAATATATATATGCTGACCCCA 2776
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OY 2114 GGAAC---GGGCGCGCATGSGTGAATGCTGACTACCTAGCTGCGCTGGCATCCGCTGGTGC 2170
Db 2777 GTGGCTTGATCTCCCATGGAGATGTTGAGTACCTTGAAAGCAATTCAGACCATCGTGA 2836
OY 2171 TTCCCATTGCCCTACGAGTTTAAACCAGAACTGGTGTGCTGCAGCTGCTTGGATGCTG 2230
Db 2837 AGCCTGTGGCCAAAGATTGATCCAGACATGCTCTAGTATCTGTGATTTGATGAT 2896
OY 2231 CACGGGGGGA-----TCGGCTGGGGGCGCTGCCAGGTGCACCTGAGGGTTAAGCCACC 2284
Db 2897 TGAAGGGCCACACCCCTCTCTAGSAGGGTACAAAGTGACGGCAAAATGTTTGGTCATT 2956
OY 2285 TCACCCACCTGTGATGSGGCTTGCCAGTGGCCGCAATATCTTATCCTAGAGGTGGCT 2344
Db 2957 TGACGAAGCAATTGATGACATTTGGCTGATGGACGTGTGTGGCTCTAGAGGAGGAGC 3016
OY 2345 ATAACTGACATCCATCTCAGAGTCCATGCGTGCACCTGCGCCCTCCCTGGAGA 2402
Db 3017 ATGATCTCACAGCCATCTGTGATGATGATCAGAAAGCCTGTGTAAATGCCCTTCTAGGAAA 3074

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Search completed: June 13, 2003, 19:26:23
 Job time : 490 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 18:39:12 ; Search time 4467 seconds
(without alignments)
13226.133 Million cell updates/sec

Title: US-09-800-187-5

Perfect score: 3648
Sequence: 1 atgacctcaacgcgcagga.....atagcccccacacacataa 3648

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:*
1: em_estda:*
2: em_esthum:*
3: em_estln:*
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5: em_estov:*
6: em_estpl:*
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8: em_hic:*
9: gb_est1:*
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23: em_gss_mam:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1298.4	35.6	1688	11	BC013219 Homo sapi
2	992.4	27.2	1006	9	AL560928 AL560928
3	876.2	24.0	998	9	AL530414 AL530414
4	799.6	21.9	1155	13	BI918415 BI918415
5	790.6	21.7	945	9	AL539258 AL539258
6	763.6	20.9	1019	14	BM921804 BM921804

7	756	20.7	807	9	AU132867	AU132867
8	732.8	20.1	739	9	AU132840	AU132840
9	725.2	19.9	993	9	AL560896	AL560896
10	719.6	19.7	879	9	AL553865	AL553865
11	710.4	19.5	771	13	BI766230	BI766230
12	687.8	18.9	707	9	AU132214	AU132214
13	684	18.8	727	9	AU142214	AU142214
14	682.8	18.7	909	14	BQ962468	BQ962468
15	682	18.7	994	12	BE734789	BE734789
16	679.8	18.6	797	10	BE541123	BE541123
17	650.2	17.8	842	10	BE541123	BE541123
18	644	17.7	690	10	AV653323	AV653323
19	642.8	17.6	856	12	BF528502	BF528502
20	633	17.4	633	14	BQ638151	BQ638151
21	632.6	17.3	718	12	BG819867	BG819867
22	631.2	17.3	1637	10	AW342122	AW342122
23	628.2	17.2	638	9	AU129981	AU129981
24	625.4	17.1	731	10	BE255457	BE255457
25	613	16.8	795	14	BM963674	BM963674
26	602.2	16.5	743	9	AU117930	AU117930
27	600	16.4	670	12	BE544016	BE544016
28	599	16.4	779	10	BE543421	BE543421
29	595	16.3	725	9	AU142216	AU142216
30	593	16.3	852	14	BQ179429	BQ179429
31	587.4	16.1	965	9	AL567746	AL567746
32	579.6	15.9	922	9	AL530413	AL530413
33	563	15.4	597	10	AM957772	AM957772
34	555.4	15.2	707	13	BI562296	BI562296
35	540.2	14.8	850	9	AL566255	AL566255
36	530.4	14.5	588	12	BE684279	BE684279
37	526.4	14.4	690	14	BQ572071	BQ572071
38	517.6	14.2	867	9	AL553840	AL553840
39	511	14.0	602	9	AL703663	AL703663
40	510	14.0	519	10	AM246112	AM246112
41	508.2	13.9	549	9	AL045483	AL045483
42	505	13.8	687	10	AV649284	AV649284
43	505	13.8	1145	13	BM466304	BM466304
44	501.2	13.7	633	13	BI917475	BI917475
45	496.8	13.6	523	13	BI011036	BI011036

ALIGNMENTS

RESULT 1
LOCUS BC013219 1688 bp mRNA linear HTC 27-AUG-2001
DEFINITION Homo sapiens, clone IMAGE:4149706, mRNA.
ACCESSION BC013219
VERSION BC013219.1 GI:15301482
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1688)
Strausberg, R.
Direct Submission
Submitted (27-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK COMMENT
Contact: MGC help desk
Email: cgepds-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalob@bcm.tmc.edu

Life Technologies. Contact : Peng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT 179 a 307 c 291 g 229 t

Query Match 27.2%, Score 992.4; DB 9; Length 1006;
Best Local Similarity 99.8%; Pred. No. 2.5e-244;
Matches 1004; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1389 CTGGAGAGCCCTCTGCTCCCAATCCGACATGCGCAAGTCTGACAGAGGCT 1448
DB 1 CTGGAGAGCCCTCTGCTCCCAATCCGACATGCGCAAGTCTGACAGAGGCT 60

QY 1449 GGTCTATGACCAAAATATGATGATCACTGCACTTGTGGACAGCCACCCCTGAGGT 1508
DB 61 GGTCTATGACCAAAATATGATGATCACTGCACTTGTGGACAGCCACCCCTGAGGT 120

QY 1509 ACCCGACGCGATCTTGGGATCATGTGCGTGGAGAGAGTGGGCGCTTGGCGGCGCTG 1568
DB 121 ACCCGACGCGATCTTGGGATCATGTGCGTGGAGAGAGTGGGCGCTTGGCGGCGCTG 180

QY 1569 CCTCACCCCTGACACCGCGCCCTGCCACAGAGCTGAGCTGCTACCTGTCACAGTCTGA 1628
DB 181 CCTCACCCCTGACACCGCGCCCTGCCACAGAGCTGAGCTGCTACCTGTCACAGTCTGA 240

QY 1629 GATGCTGGGCTCATCTCGGGGCGACAGAGAAATGAAAAACCGGAGCTGCAACCTGAGAG 1688
DB 241 GATGCTGGGCTCATCTCGGGGCGACAGAGAAATGAAAAACCGGAGCTGCAACCTGAGAG 300

QY 1689 TTCCAACTTGAATCCATCTATATCTGCGCCAGTACCTTGCCTGTGTGACAGCTTGCAC 1748
DB 301 TTCCAACTTGAATCCATCTATATCTGCGCCAGTACCTTGCCTGTGTGACAGCTTGCAC 360

QY 1749 TGGCGCTGCTGCGCGCTGGGAGGCGTGTCTGACAGAGAGTTCGATGGTCTGC 1808
DB 361 TGGCGCTGCTGCGCGCTGGGAGGCGTGTCTGACAGAGAGTTCGATGGTCTGC 420

QY 1809 TGTGTGCTGCTGCCACAGACACACAGACAGAGATGACAGCTTGGGTTTGTGTTT 1868
DB 421 TGTGTGCTGCTGCCACAGACACACAGACAGAGATGACAGCTTGGGTTTGTGTTT 480

QY 1869 CAACCTGTGCTGTGCTGCTGCGCATGCGCCAGACTATCACTAGTGGGATGCGCTAAGGAT 1928
DB 481 CAACCTGTGCTGTGCTGCTGCGCATGCGCCAGACTATCACTAGTGGGATGCGCTAAGGAT 540

QY 1929 CCTGATTTGGATTTGGATTTGATCCACACCGTATGATGAACTGACAGCATGTTTGAAGATGA 1988
DB 541 CCTGATTTGGATTTGGATTTGATCCACACCGTATGATGAACTGACAGCATGTTTGAAGATGA 600

QY 1989 CCCGAGTGTGATATGATGCTGCTGACAGCGTATGATGAGGCACTTCTCCCAATGAGG 2048
DB 601 CCCGAGTGTGATATGATGCTGCTGACAGCGTATGATGAGGCACTTCTCCCAATGAGG 660

QY 2049 GGATGAGGCTGCGACAGCAGCATGCGCGGCTGCGGAGCAGAGGCTTCAACCGTCAAGT 2108
DB 661 GGATGAGGCTGCGACAGCAGCATGCGCGGCTGCGGAGCAGAGGCTTCAACCGTCAAGT 720

QY 2109 GGCATGGAACGGGCGCCGATGGGTATGCTGACTACCTAGTGCCTGCGATGCGCTGCT 2168
DB 721 GGCATGGAACGGGCGCCGATGGGTATGCTGACTACCTAGTGCCTGCGATGCGCTGCT 780

QY 2169 GCTTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2228
DB 781 GCTTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

QY 2229 TGCAC-GGGGGGATGCGTGGGGGCTGCGAGGCTGCACTGAGGTTTGAAGGCTCA 2287
DB 841 TGCACGGGGGATGCGTGGGGGCTGCGAGGCTGCACTGAGGTTTGAAGGCTCA 900

QY 2288 CCCACTGCTGATGGGCTTGCAGATGCGCGCATATCTTATCTTATGAGAGGTGCTATA 2347

DB 901 CCCACGCTGATGGGCTTCCAGTGGCCGACATATCTTATCTTACAGAGGTGCTATA 960

QY 2348 ACCTGACATCCATCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2393

DB 961 ACCTGACATCCATCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006

RESULT 3
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LOCUS
DEFINITION
AL530414 LFL NFL001.NBC4 Homo sapiens cDNA clone CS0DD007YC02 5
prime, mRNA sequence.
AL530414
VERSION
AL530414.1 GI:12793907
KEYWORDS
EST.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 998)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: secre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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/clone="CS0DD007YC02"
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/sex="male"
/issue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Peng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT 239 a 277 c 265 g 212 t 5 others

Query Match 24.0%; Score 876.2; DB 9; Length 998;
Best Local Similarity 99.2%; Pred. No. 2.2e-214;
Matches 898; Conservative 3; Mismatches 2; Indels 2; Gaps 2;

QY 1 ATGACCTCAACCGGAGGATTCACACCAACGAGGAGGAGAGTATGAGCAACCCC 60
DB 18 ATGACCTCAACCGGAGGATTCACACCAACGAGGAGGAGAGTATGAGCAACCCC 77

QY 61 CAGTGCCTTATCCCAATCTAGCGGAGGTAAAGAAAGGCAAAATGAAGAGCTGCGC 120
DB 78 CAGTGCCTTATCCCAATCTAGCGGAGGTAAAGAAAGGCAAAATGAAGAGCTGCGC 137

QY 121 CCCGCTTATCCCAATCTAGCGGAGGTAAAGAAAGGCAAAATGAAGAGCTGCGC 180
DB 138 CCCGCTTATCCCAATCTAGCGGAGGTAAAGAAAGGCAAAATGAAGAGCTGCGC 197

QY 181 CAAGAATGGAAGAGACCTATCTGAGCTGCAAGGATGATGCAACCTTGAGGCT 240
DB 198 CAAGAATGGAAGAGACCTATCTGAGCTGCAAGGATGATGCAACCTTGAGGCT 257

QY 241 GAAGCAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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High quality sequence stop: 825.

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/clone_11b="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: Notif; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 294 a 315 c 348 g 198 t

ORIGIN

Query Match 21.9%; Score 799.6; DB 13; Length 1155;
Best Local Similarity 97.8%; Pred. No. 1.3e-194;
Matches 843; Conservative 0; Mismatches 14; Indels 5; Gaps 3;

301 TGGATGACAGCTTCCCGAAGGCGCTGAGGCGCTCCATCCATCAAGAGCACTATC 360
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361 CAGAGAGGCGCTTCTAGATGCTGCGTCTTTCAGGCGCGGTTGCTGAAAAGAGAG 420
378 CAGAGAGGCGCTTCTAGATGCTGCGTCTTTCAGGCGCGGTTGCTGAAAAGAGAG 437
421 CTGATGTTGGTTCACAGCCTAGAAATATATATGATGATGGAACAAACCCAGTATGAT 480
438 CTGATGTTGGTTCACAGCCTAGAAATATATATGATGATGGAACAAACCCAGTATGAT 457
481 GAGGAGAACTCCGCTGCTAGACAGACACCTAGACACTAGTTATGCTGCAACTCA 540
498 GAGGAGAACTCCGCTGCTAGACAGACACCTAGACACTAGTTATGCTGCAACTCA 557
541 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
558 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 617
601 GCTGAGATCCGGAATGCGATGCGCATTTAGGCGCTCTGAGACATACGCGCCAGCAGT 660
618 GCTGAGATCCGGAATGCGATGCGCATTTAGGCGCTCTGAGACATACGCGCCAGCAGT 677
661 CTATGATGCTATTTGATGCTTCAACACAGTGGCTGTGGACGCCGTATGCTCAACAG 720
678 CTATGATGCTATTTGATGCTTCAACACAGTGGCTGTGGACGCCGTATGCTCAACAG 737
721 AAACACCGCATCCGAGAGGCGCTTATCGATGTT-GGATGTGACACACAGGTCAGAAAC 779
738 AAACACCGCATCCGAGAGGCGCTTATCGATGTTGGATGTGACACACAGGTCAGAAAC 797
780 ACAGTTCACCTTCGACGACGAGACCCAGATGCTCTATTCTTCATCACCAGCTACAGCA 839
798 ACAGTTCACCTTCGACGACGAGACCCAGATGCTCTATTCTTCATCACCAGCTACAGCA 857
840 GGGTATGCTTGGGCGCCACCTGAGAGGCGCTCAACTGAGTGGTCCACACAGTTTGGCCAGG 899
858 GGGTATGCTTGGGCGCCACCTGAGAGGCGCTCAACTGAGTGGTCCACACAGTTTGGCCAGG 916
900 CCAAG 904
917 CMAAG 921

RESULT 4
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DEFINITION 603176195F1 NIH_MGC_121 Homo sapiens cDNA IMAGE:5240639 5',
B1918415
ACCESSION B1918415
VERSION B1918415.1 GI:16182107
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1155)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strusberg, Ph.D.
Email: cgarbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1606 row: m column: 24
High quality sequence start: 29

2498 GCTTACGGGTGATGAGTGAAGACAGAGAGGACCCCTCAGTCTAAGTTGGTCACCA 2557
32 GCTTACGGGTGATGAGTGAAGACAGAGAGGACCCCTCAGTCTAAGTTGGTCACCA 91
2558 AGAAGGACACCCCAACACGACCAACCTAGTATGAGCGGATGACACACAGAGAAAGA 2617
92 AGAAGGACACCCCAACACGACCAACCTAGTATGAGCGGATGACACACAGAGAAAGA 151
2618 AGTTCTGAGAGCAGGCGATGGGGAAGTCACTTGGGCAATTTGGGGAAGTCCACTC 2677
152 AGTTCTGAGAGCAGGCGATGGGGAAGTCACTTGGGCAATTTGGGGAAGTCCACTC 211
2678 CAGGCGCAGTACTGAGAGCAGTGTGGGCGCTTACACAGGACCGCCCTCAGAGG 2737
212 CAGGCGCAGTACTGAGAGCAGTGTGGGCGCTTACACAGGACCGCCCTCAGAGG 271
2738 CAGGCGCAGTACTGAGAGCAGTGTGGGCGCTTACACAGGACCGCCCTCAGAGG 2797
272 CAGGCGCAGTACTGAGAGCAGTGTGGGCGCTTACACAGGACCGCCCTCAGAGG 331
2798 TGGTGGGACACACCTCAGAGAGGCTGTGGGGAAGCCACTCCGACACGACCACT 2857
332 TGGTGGGACACACCTCAGAGAGGCTGTGGGGAAGCCACTCCGACACGACCACT 391
2858 CAGAGAGACTGTGGGGAAGGAGCCATTCTGACACGACCACTCAGAGAGATGCTTGGG 2917
392 CAGAGAGACTGTGGGGAAGGAGCCATTCTGACACGACCACTCAGAGAGATGCTTGGG 451
2918 GAGCCAGCTGGGACACCTCAGAGAGGCTGTGGGGAAGCCACTCAGAGAGATGCTTGGG 2977
452 GAGCCAGCTGGGACACCTCAGAGAGGCTGTGGGGAAGCCACTCAGAGAGATGCTTGGG 511
2978 CCATCTCGAGAGGAGCCATGAGGAGGACCACTGACACGACCACTCAGAGAGGCTC 3037
512 CCATCTCGAGAGGAGCCATGAGGAGGACCACTGACACGACCACTCAGAGAGGCTC 571
3038 CAGGCGGACACGCTGATGCAAACTCTTACGCTGAGAGCAGACACCAAGATCCGCC 631
572 CAGGCGGACACGCTGATGCAAACTCTTACGCTGAGAGCAGACACCAAGATCCGCC 631
3098 CAACCTCAGCTGAGAGGAGTACACCCAGATATCCAGATACCTGATGAGGAGTTC 3157
632 CAACCTCAGCTGAGAGGAGTACACCCAGATATATCTCCAGATACCTGATGAGGAGTTC 691
3158 TGAAGACCTTGAAGTACAGGAGGAAATCTCAGAGGAGGCTCAGAAATCTCAGAGGAG 3217
692 TGAAGACCTTGAAGTACAGGAGGAAATCTCAGAGGAGGCTCAGAAATCTCAGAGGAG 751

OY 3218 AGGAGNACCTACTAGGAGAGGAGCTGAGGTCAGAGC--ATGGCTGATTCGATCTGAT 3275
 DB 752 AGAGAGACCTACTAGAGAGGAGGAGCTGAGAGTCAGGACCAATGGCTGATAGATGAT 811
 OY 3276 GCAGGAGATCTAGGAGGAGCTGATCAGGACCAATTTTAT-GGCTGACACCACTG--CC 3332
 DB 812 GCAGGAGATCTAGGAGGAGCTGATCAGGACCAATTTTATGGCTGATGACACCACTGAGCC 871
 OY 3333 CTGCTGCTCCCAATTTGGTGCA 3354
 DB 872 TTGTCTCCCAATTTGGTGCA 893
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 ACCESSION AL539258.1 GI:12868309
 VERSION AL539258.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 945)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 /clone_1lb="LTL_FL013_Pbrn1"
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 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by Life
 Technologies. Contact: Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 173 a 277 c 276 g 213 t 6 others
 ORIGIN
 Query Match 21.7%; Score 790.6; DB 9; Length 945;
 Best Local Similarity 98.7%; Pred. No. 2.4e-192;
 Matches 816; Conservative 2; Mismatches 6; Indels 3; Gaps 2;
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 DB 1 AAGGACCTCTGGAGAGCCCTGCTGCTCCCAATCCGATGAGGACGCTGACAGTCTCGA 60
 OY 1442 CAGGGCTGCTTATGACCAAAATATGATGATCACTGCACTTGGGACAGCACCACC 1501
 DB 61 CAGGGCTGCTTATGACCAAAATATGATGATCACTGCACTTGGGACAGCACCACC 120
 OY 1502 CTGAGGTATCCCAAGCAGCATCTGGGATCATGTGCGCTGAGAGAGCTGGGCTTGGCG 1561
 DB 121 CTGAGGTATCCCAAGCAGCATCTGGGATCATGTGCGCTGAGAGAGCTGGGCTTGGCG 180
 OY 1562 GGGCTGCGCCACCCCTGACACCCGCGCTGACACAGAGGCTGAGTCTGCTACCTGTACA 1621

DB 181 GCGCTGCTCAGACCTGACACCCGCGCCGACACAGAGGCTGATCTCACCCTGCACA 240
 OY 1622 GTGCTGATCTAGGCTGATCTCCGCGCCAGAGAGAAATGAAACCCGGAGCTGCACC 1681
 DB 241 GTGCTGATCTAGGCTGATCTCCGCGCCAGAGAGAAATGAAACCCGGAGCTGCACC 300
 OY 1682 GTGAGATCTCAACTTATGATCTATATGATGATGATGATGATGATGATGATGATGATGAT 1741
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 DB 361 TTGGCACTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 OY 1802 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1861
 DB 421 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 OY 1862 GCTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1921
 DB 481 GCTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 OY 1922 TACGATCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1981
 DB 541 TACGATCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 OY 1982 AGATGACCCCAAGTGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2041
 DB 601 AGATGACCCCAAGTGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 OY 2042 CCATGAGGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 2101
 DB 661 CCATGAGGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 720
 OY 2102 TCAACGCGCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2161
 DB 721 TCAACGCGCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 OY 2162 GCCTGCTGCTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2208
 DB 781 GC--TGCTGCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
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 LOCUS BM921804 AGENCOURT_6706889 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753394
 DEFINITION 5', mRNA sequence.
 ACCESSION BM921804
 VERSION BM921804.1 GI:19372183
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1019)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LLM12789 row: b column: 19
 High quality sequence stop: 725.
 Location/Qualifiers
 1. 1019
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 source

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/note="Organ: pooled brain, lung, testis; Vector:  
pCMV-Sport6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 65. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research genetics tracking code  
021. Note: this is a NIH/MGC library."  
278 c 250 g 198 t 5 others
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Query Match	20.9%	Score 763.6	DB 14	Length 1019
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Db 91	ATGACCTCAACCGCGCAGAGATTCCACCAACACGAGCGAAGAGTAGGCGAGAACCC	150		
QY 61	CAGTGGCCCCCTCAAGACTCCAGTGTCACTTCGAAAGCAAAATATTTAAAAAGGAGCCGTT	120		
Db 151	CAGTGGCCCCCTCAAGACTCCAGTGTCACTTCGAAAGCAAAATATTTAAAAAGGAGCCGTT	210		
QY 121	CCCCGCTTATCCCCCAATCTAGCGGAGGTAAAGAAAGCAAAATAGAGAGCTCGGC	180		
Db 211	CCCCGCTTATCCCCCAATCTAGCGGAGGTAAAGAAAGCAAAATAGAGAGCTCGGC	270		
QY 181	CAAGCAATGAGAAAGACCTAATCGTGGAGCTGCAAGGATGAGATCTGAACCTTAGAGCT	240		
Db 271	CAAGCAATGAGAAAGACCTAATCGTGGAGCTGCAAGGATGAGATCTGAACCTTAGAGCT	330		
QY 241	GAAACACCTGGCTGGCACCTGCGCTTGGTGTGGATGACAGTTAAATGAATTCATTGCTC	300		
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Db 391	TGGGATGACACCTTCCCGAAGGCCCTAGGCGGCCCATGGCATCAGAGCAACTGATC	450		
QY 361	CAGAGAGGCCCTCTAGATCGCTGCGTGTCTTCAGGCCCGGTTTGTGTAAGAAAGAAAG	420		
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Db 631	TACCTCCGTGCTGCTGCGCTCAGGCTCTTCTCAGGCTGGTGGATGCGGCTCTGGGG	690		
QY 601	GCTGAGATCCGGAATGGCATAGGCCATATAGGCGCTCTGGCAATCAAGCCGCAAGT	660		
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QY 721	AAACACCGCATCCGGAGGAGGCTTATATGAGAGT - GGAATGTGACCAACAGGTCAAGAA	778		
Db 811	AAACACCGCATCCGGAGGAGGCTTATATGAGAGTGGGGGATGTGACCAACAGGTCAAGAA	870		

Qy	779	CACAGTTCACCTT	791
D _b	871	CACAGNTCACCTT	883

RESULT 7	
AU132867	
LOCUS	AU132867 807 bp mRNA linear EST 01-AUG-2002
DEFINITION	AU132867 NT2RP4 Homo sapiens cDNA clone NT2RP4000749 5', mRNA sequence.
ACCESSION	AU132867
VERSION	AU132867.1 GI:10993406
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 807)
AUTHORS	Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuno,Y. and Isogai,T.
TITLE	HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,T., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuno,Y., Isogai,T.)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Isogai

Genomics Laboratory
Helix Research Institute
153-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES	Location/Qualifiers
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/notes="Vector: pME18SFL3: mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

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	Matches 78;	Conservative 0;	Mismatches 13;	Indels 3;	Gaps 2
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QY	352	CAACTGATCCAGGAGGGGCTCTCAGATCGGTGGCTGCTTCAAGGGCCGGTTGGCTAA	411		
Db	61	CAACTGATCCAGGAGGGGCTCTCAGATCGGTGGCTGCTTCAAGGGCCGGTTGGCTAA	120		
QY	412	AAGGAAGAGCTGATGTTGGTTCAACAGCCTAGAAATATTTGATCGATGGAACAACCGAG	471		
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QY	472	TACATTAATGAGGAGAGAACTCGGTGCTTGAAGACACCAACAGACAGTAACTGAT	531		
Db	181	TACATTAATGAGGAGAGAACTCGGTGCTTGAAGACACCAACAGACAGTAACTGAT	240		
QY	532	CCGAACCTACTCTGTGCTGACCTGAGCCTCAGAGCTGTGCTCAGCGTGGTAGATCG	591		
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[illegible]

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/note="Organ: pooled lung and spleen; Vector: pcMV-SpO86
Site.1: NotI; Site.2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note
this is a NIH.MGC Library."

BASE COUNT      193 a      243 c      219 g      116 t
ORIGIN

Query Match      19.5%; Score 710.4; DB 13; Length 771;
Best Local Similarity 97.5%; Pred. No. 1e-171;
Matches 753; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

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QY      2447  CCTGGCCTCAATCACTAGAGACCAATCCAAATGCATCGCAGATCTGGGCGAGCTTACCGG 2508
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Db      181      TCATGAGAGTGAAGACAGAGAGAGACCCCTCCAGTTCTTAAGTGGTGTCCCAAGAGGCAC 240

QY      2567  CCCAACCCGCAAAACCTAGGTTACTCTGGGGAGAGACCAACAGGAAAGAAAGGTTCTGG 2626
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QY      2627  AAGCAGGCGATGGGAAAGTCACTCTGCGCATCTATTGGGGAAAGAGTCCACTCCAGCCAGA 2686
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QY      2807  AGACCACTCAGAGAGAGAGGTGTCTGGGGGAGCCACTCCGAGCAAGACCACTCAGAGGAGA 2866
Db      481      AGACCACTCAGAGAGAGAGGTGTCTGGGGGAGCCACTCCGAGCAAGACCACTCAGAGGAGA 539

QY      2867  CTGTGGGAGAGAGCCATTCTGGACCAAGACCACTTCAGAGATGTCTGTTGGGGAGCCACGC 2926
Db      540      CTGTGGGAGAGAGCCATTCTGGACCAAGACCACTTCAGAGATGTCTGTTGGGGAGCCACGC 599

QY      2927  TGGGCGCAGATCTACCTCAGAGAGAGGTGTAGAGAGAGTAA-ACGTGGCCAGACATCTCG 2985
Db      600      TGGGCGCAGATCTACCTCAGAGAGAGGTGTAGAGAGAGTAAACTGTGGCCAGACATCTCG 659

QY      2986  GAGGACACCATTGAGAGGAGGACCACTAGCACTAGCACTAAGTCAAGAGAGAGCTCCAGGGGC 3045
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QY      3046  ACCGAGCTGATCCAAACTCTCTTAGCCTGAGACACAGACCAACGACCCCGC 3097
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Db 719 ACCGAGCTGATCCAAATCTCTAGCTCTCCACGACGACGACACGAGAACCCCCC 770
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 version AUI32214.1 GI:10992568
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 REFERENCE 1 (bases 1 to 707)
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 Iwagaki, T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Iwagaki
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genom@seintl.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
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 /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
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 Oy 1777 GTGCTTCACAGAGAGTTCGAATGAGTGTGCTGTGTGTGCGTCCCGCAGGACACACAGCA 1836
 Db 121 GTGCTTCACAGAGAGTTCGAATGAGTGTGCTGTGTGTGCGTCCCGCAGGACACACAGCA 180
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Dd	540	GAACGTGCTGCTGCTCTAGCTGCTTGTATGCTGCACAGGGGGATCGCTGGGGGCTGC	599
QY	2257	CAGGTGCACCTGAGGGGTTATGGCCACTCACCCACCTGCTGATGAGGCTTGGCAATGCG	659
Dd	600	CAGGTGCACCTGAGGGGTTATGGCCACTCACCCACCTGCTGATGAGGCTTGGCAATGCG	659
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VERSION	AU142214.1	GI:11003735	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
TITLE	1 (bases 1 to 727)		
JOURNAL	Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T.,		
COMMENT	Nishikawa,T., Nakamura,Y., Sugano,S., Masuno,Y. and Isogai,T.		
	HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S.,		
	Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.,		
	Masuno,Y., Isogai,T.)		
	Unpublished (2000)		
	Contact: Takao Isogai		
	Genomics Laboratory		
	Helix Research Institute		
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan		
	Tel.: 81-438-52-3975		
	Fax: 81-438-52-3986		
	Email: genomics@hri.co.jp		
	HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix		
	Research Institute; cDNA library construction: Department of		
	Virology, Institute of Medical Science, University of Tokyo, and		
	Helix Research Institute.		
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	/note="Vector: PMB18SFJ3; primary endothelial cells"		
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Matches	698; Conservative 0; Mismatches 7; Indels 1; Gaps 1;		
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DEFINITION 601568905F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843552 5',
ACCESSION BE734789
VERSION BE734789.1 GI:10148781
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 994)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cygabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubln Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov
Plate: LNC338 row: J column: 01
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/note="Organ: Placenta; Vector: pORF7; Site_1: XhoI;
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Directionally cloned into EcoRI/XhoI sites using the
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for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 226 a 285 c 325 g 158 t
ORIGIN
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Matches 751; Conservative 0; Mismatches 8; Indels 6; Gaps 6;
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DB 222 GACCATTTCTGAGGAGCCATTTGGGGAGCCATGCTGGGCCAGACCACTCAGAGAGGC 281
QY 2826 TGTGGGGGAGGAGCCATTCGGACACCACTCAGAGAGACTGTGTGGAGAGCCATTCT 2885
DB 282 TGTGGGGGAGGAGCCATTCGGACACCACTCAGAGAGACTGTGTGGAGAGCCATTCT 341
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DB 462 CACACTGAGACCACTACACTCAGAGAGAGGCTCCA-GGGGACACCGAGCTGATCCAAATCC 520
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